

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCTCGACCTCGA
CCCACCGTCCGGGCCGGAGCAGCACGGCGCAGGACCTGGAGCTCCGGCTCGTCTCCG
CAGCGCTACCCGCCATGCCCTGCCGCCGGCGCAGGACCTGGAGCTCCGGCTCGTCTCCG
CTGCTGCCGCCGGCGCCGGAGGCGCCAAGAACGCCAGGCCCTGCCACCGGTGCCGGGGCT
GGTGGACAAGTTAACAGGGGATGGTGACCCGAAGAACAGAAACTTTGGCGGCGGAAACA
CGGCTGGGAGGAAAAGACGCTGTCAAGTAGCAGTCAGCAGGAGATTGCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCAGTCAGATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGCGACGGGCTCTGCCGCCGCACATGGGGTACCAAGGCCGCTGTGACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACAGTCC
TGCAAGACGTGCTCGGCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGATGTGGACGAGTGTGCGGGCGAGCCGCCCTGCAGCGCTG
CCGAGTTCTTAAGAACGCCAACGGCTCTACAGTGCAGAGACTGTGACTCCAGCTGTG
GGCTGCACAGGGAAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGCTACTAGCAGAAAAAAACCTGTGAGGAAAAACG
AAAATGCTACAAACTCAGGGAGCTACGTCTGTGTGCTGACGGCTTCGAAGAACG
GAAGATGCCTGTGCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACAGCT
GCCCTCCCGCAAGACCTGTATGTGCCGACTTACCCCTAAATTATTCAAGAGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGCTCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCATTTGCCCTAAACAGCTGCATTCTGGTTGTCTTA
AACAGACTTGTATATTGTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAAATCAGG
AGGAAAAAAAGGGCGCCCGCAGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCAACCTGTTATTGCACTGCATTCTAGTTGTGTTGTCAAAC
TCACAAATTCAAAATAAGCATTTCATGCTGGATCGGAATTAACTCGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTTCTGAGGGAGAACAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLP RRA ALG I LP L L L PPAPEAA KPTP C H R C R G L V D K F N Q G M V D T A K K N F G G G N T A W E E K T L S K Y E S S E I R L
L E I L E G L C E S S D F E C N Q M L E A Q E E E L E A N W L Q L K S E Y P D L F E W F C V K T L K V C C S P G T Y G P D C L A C Q G G S Q R P C S G
N G H C S G D G S R Q G D G S C R C H M G Y Q G P L C T D C M D G Y F S S L R N E T H S I C T A C D E S C K T C S G L T N R D C G E C E V G W V L D E
G A C V D V D E C A A E P P P C S A A Q F C K N A N G S Y T C E E C D S S C V G C T G E G P G N C K E C I S G Y A R E H G Q C A D V D E C S L A E K T
C V R K N E N C Y N T P G S Y V C V C P D G F E E T E D A C V P P A E A E A T E G E S P T Q L P S R E D L

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

00014074-05820690

FIGURE 3

CAGGTCCAATGCACTCGGTTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTC
GACCTGACCCACGGTCCGCCAGGCCGGAGGCAGGCCAGCTAAACGGAAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGGTGCCTAGGTGC
GCACGAGGAGTTTCCGGCAGCGAGGGCTGAGCAGC**ATGGCCCGAGGAGCGCCCTC**
CTCTGGCGCCGCGAGGGAGCTGACCTATGGATCGATGCTCACAGGCAAGACTCA
TAGGATTGAAAGAAGATATCTGATTGTTAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGCAAAGAGAAATGCCAGCTTCCCTGCAATATCCATTCCATGAAATTTCAC
CTGGCAAGCTGCAGGGCAGGAATACTCTATGAAATTCTGTCTTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGCTCTGTGGAACAGTGCCTACAAGGC
TCAGTTGTCAGTTGTTTCCATGTCAGGAAAACAGGATGGGGTGCAGCATTTGA
GGATGTGATTGTTATGAAATTGAGGCAACACCATTCTCCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAAACAGCTGAGTGCCTGGGGCAGGCTGGCAATGGAGGTTTGTAA
GAAAGACGCATCTGCGAGTGTCTGTGGTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCCAGGTATGAAATGGGAGACTTGTGACTCTGGGTTCTGCATCTGCCAACCTG
GATTCTATGGAGTGAACATGTCACAAAGCCTACGTCACCCACTGCTTAATGGAGGGACC
TGTTCCTACCTGGAAAATGTTGCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCAACACCTGTCGAAATGGAGGAAATGCACTGGTAAAGCAGGAAATGTAAGTGT
CCAAAGGTTACAGGGAGACCTCTGTTCAAGCCTGTGCGAGGCTGGCTGGCACAT
GGAACCTGCCATGAAACCCAAATGCCAAATGCAAGGGTTGGCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGGGGCCAGTCAGGCAGC
ACACGCCCTCACTTAAAGGCCAGGAGGCCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAAGTACACCAAGTCTAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCACTAACACTTAAAGAATACTGGCTGAATTATAGCT
TCATTATAAATCACTGAGCTGATATTACTCTCTTAAAGTTCTAAGTCACTGTGAG
CATGATGGTATAGATTCTGTGTTCAAGTGGCTGGGACAGATTATATTATGTCATTGA
TCAGGTTAAAATTTCAGTGTGAGTTGGCAAGATATTCTAAAATTACATGCAATTGTT
GTCTGGGGCAGGGAACATCAGAAAGGTTAAATTGGGAAAAATGCTGAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTAAGTTACAGCATTCTCAGATTATCTCAGATATTAGAT
GTTGTTGAATCTTAAAATTGCTCTTAATTTTAAACTCTCAATACAAATATATTGACC
TTACCAATTCCAGAGATTCTCAGTATTAAAAAAATTACACTGTGGTAGGGCATTT
AAACAATATAATATATTCTAAACACAATGAAATAGGGAAATATAATGTAAGTCACTTTTGCA
TGGCTTGAAAGCAATAATATTGTAACAAACACAGCTTACCTAATAAACATTTAT
ACTGTTTGTATGTTAAAGGTGCTGCTTGTGTTAGTTTTGGAAAAAA
AAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGCCCAACTTGTTTATGCACTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIMNSEGNTILQTPQNIAFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKICCPPGLEGEQCEISKCPQPCRNGGKICGKSCKCSKGYQGDLCSPKVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

T00740-35820660

FIGURE 5

CGGACGCGTGGCGTCGGCGGTGCGAGAGCCAGGGAGGCAGGGCGCGGGCAGCTGGG
CCCCAGCCCACACCTTCACCAAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGGCCACTGGCTCTGGGTGCCCCAGCAGGGCTGTGGGCCGG
GAGCTAGCACCGGGTCTGCACCTGGGGCATCCGGGACGCGGGAGGGCGGTACTGCCAGGA
GCAGGACACTGTGCTGCCGCGCTGCCGAGCAGCTGTGCCCTACCTGGGCCATCT
GTTACTGTGACTCTTCTGCAACCGCAGGCTCCGACTGTGCCCTGACTCTGGGACTTC
TGCCTCGGCTGCCACCCCTTTCCCCGATCCAAGGATGTATGATGGAGGTCTATCTA
TCCAGTCTGGGAACGTACTGGGACAACTGTAAACCTGGCACCCTGCCAGGAGAACAGGCAGT
GCCATGGTGATCCAGACATGATAAAGGCCATCAACCCAGGCAACTATGGCTGCCAGGCTGG
GAACCACAGGCCCTCTGGGCATGACCTGGATGAGGGCATTGCTACCGCCCTGGCACCA
TCCGGCCATCTCCCTGGTCATGAAACATGATGAAATTATACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCTGGGCCCTGAGAAAGTGGCCCAACCTGATTICATGAGCTCTTGA
CCAGGCAACTGTGAGGCTCTGGGCCCTTCCACAGCAGCTGGCATCCGATCGTGTCT
CAAATCCATTCTCTGGGACACATGACGCCCTGCTCTGTCGCCAGAACCTGCTGTCTGGTGCAC
ACCCACAGGCCAGGGCTGCCGCGTCTCGATGGTGGCTTCTGGTGGTTCTGGCTCG
CCGAGGGGTGTGCTGACTGACCATCTGACAGCCAGGCCATGGTGGGCCAGGCCAGGGCAGTGC
CTGCGCCCCCTGTATGATGACAGCCAGGCCATGGTGGGCCAGGCCAGGGCAGTGC
CACTGGCCCAACAGCAGTGTAAACAATGACATCTACAGGCTGACTCTGGTGTCTACCGCCT
CGGCTCAACGACAAGGAGATCATGAGGAGCTGATGGAGATGGCCCTGTCCAAGCCCTCA
TGGAGGTGATGAGGACTCTTCTTACAAGGGAGCATCTACAGGCCACAGGCCAGTGAGC
CTTGGGAGGGCAAGAGATAACCGCCGCTGGGACCAACTCAGTCAGATCACAGGATGGGG
AGAGGAGACGGCTGCCAGATGAGGACGCTCAAAATACTGGACTGGGCCCAACTCTGGGCC
CAGGCTGGGGCGAGAGGGCCACTTCCGATCTGCGCCGGTCAATGAGTGCACATCGAG
AGCTTCGTGCTGGCGCTGGGCCGCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGGCGGTGACCCCCAGCCTGCCGAGAGGCCGGCGCAGGGCGGCCAGGGCGCCAGGGCGTAAT
CCCCGGCGCGGGTTCCGCTGACGCAAGCAGGCCCGCTGGAGGCCGGCGAGACTGGCG
GAGCCCCCAGACCTCCAGTGGGACGGGGCAGGGCCTGGGATGGAAAGAGCACAGCTGCAG
ATCCCAAGGGCTCTGGGCCCACTCAAGAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCCAACCCCAACTCCGTATTCTTTTTTTTTTTAGACAGGGCTTCTGCTCCG
TTGCCCAAGGTTGGAGTGCAGTGGCCCATCAGGCTACTCTAACCTCCGACTCTGGTTCA
AGTGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGACCCACACCTGGC
TAATTTTTGATTTTTCTAAAGAGGGGGGTCTACTGTGTTGCCAGGGCTGGTTCTGAACT
CTGGGCTCAAGCGGTCCACCTGCCCTCCCAAAGTGTGGGATTGCAAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTTCACTGTAAAAAAA
AAAAACCAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPPLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYQEQDLCCRGRADDCA
ALPYLGAICYCDLFCNRTVSDCCPFDCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

TOTAL = 258206

FIGURE 7

AGGCTCTTGGCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGACACATNACGCCCTGTCCTTNGCCCGAACCTGCTGTTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCCTGGTGGTCTCGCGTCGCCGAGG
GNTGGTGTCTGACCCTGCTACCCCTCTCGGCCGTGAACGAGACGAGGCTGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTCTTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGC ACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGA CTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGG**ATG**ACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACTCGGCTGCTGCTCTGGGACCCGGCCAGCTATAAGGCTCTGGGGGG
CCCCGCTGCAGCCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCA GTGGGAGCCTGCTGGTCTGGGACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCACCCACCCCTGACCCCTCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCCTGCAGATGGCCCTCCAACCCTCTCTGCTGCTGTTTC
CATGGCCCAAGCATTCTCACCCCTTAACCCCTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCCAACCCATCTATGACTTGAGGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGT**AA**AGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGGAGTCTCCAGAGATGGGGCTGGAGGCCCTGGAGGAA
GGGGCCAGGCCCTCACATTGCTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGD~~PASYRLWGAPLQPT~~
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSSDT
DPPADGPNPLCCCFHGP~~AFSTLN~~VLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRR~~AQ~~

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

000002853 - 07/10/2014

FIGURE 10

CCCCACGGCTCCGAACCTCTCCAGCGATGGGAGCCGCCGCTGTCCCAAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGGCGAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCCCACCGCCGAGGACGCCAACAGTTTGCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCGGGTTCCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGAAAGGCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACACTATAACGCCCTTCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCAGCGGGAGGGGCGCCCGCAGGCTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAAGCGAAGCAGTTCGAGTTGGCTCCGCCCCACCCGCGGACCAAGCGCACAC
GGCGGCCAGCCCCACTCGTAGTCTGGGAGGCAGGGGCAGCAGGCCCTGGGCCCTCCC
CACCCCTTCCCTTCTTAATCCAAGGACTGGCTGGGCTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCCGCGAAGCAGTCCGAGCCCCCAGCTGGAAAGGGCAGGCCGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCCGACGGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACAGCCTCTGCCCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCAGTGAAGGCCCTGAGACAAACCGTCTGGAGGTGGCTGTCTCAA
TCTGCTTCTGGATCTCCCTCAGTCTGCCCTCAGGCCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTTCACTCCACATTCCACGACCCAGGCCCTGACCCCCACCC
AGGGTTGTCACCTCCACATTCCACGACCCAGGCCCTGACCCCCACCCAACTCCAGGCC
CGGAATAAAACCATTTCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDGVFTIEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGGCCATCACCTGTTGCCAGTGTGGAAAAAATTCTCCCTGTTGAATTTCGACATGGAG
GACAGCAGCAAAAGGGCAACACAGGCTGATAAGACCAGAGCACGAGGGAGTTATTTCAC
CATACGCCCTCAGGACGTTCCCTAGCTGGAGTTCTGGACTTCACAGAACCCATCCAGT
CATTTTGATTTTGCTGTTATTTTTCTTTCTTTCCACCAATTGTATTTAT
TTCCCGTACTTCAGAAAATGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCT
GAAGCTTGGCTTATCATTTCCCTGGGGCTACTCACAGGTGTCAAACTCTGGCTGCC
CTAGTGTGTCGCGCTGCGACAGGAACCTTGCTACTGTATGAGCGAAGCTTGACCTCAGT
CCCTTGGGATCCCGGAGGGCTAACGCTACTCCCTCACAACAAACCAATTAAATATGC
TGGATTTCCTGAGAACTGCACAAATGTCAGCTCGGTGCACACGGTCTACCTGTATGGCAC
AACTGGACGAATTCCCATGAACCTTCCAAGAAATGTCAGAGTTCTCATTGCAAGGAAAC
AAATTACGACCATTTACGGGCTGCTTGGCCAGCTTGAAGGCTTGAAGAGCTGACCT
GGATGACAACCTCCATCACAGTGGGGGTTGAAGACGGGCTTCCGGGAGGCTATTGAC
TCAAATTTGTTTGTCTAAAGATCACCTGAGCAGTGTGCTGTGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCAGATTGCTGTATCCGACATGGCCTTCAGAA
TCTCAGGAGCTGGAGCTCTATTGTGGAGGGGAACCTCTGACCAAACAAGGGTATCGCC
AGGGCACCTTCAGCATCTACAAAGCTCAAGGAATTTCATTTGACGTAATTCTGCTG
CACCCCTCTCCGATCTCCAGGTACGATCTGATCAGGTCTATTGCAAGGAAACAGAT
AAACCAACATTCTCTTGACGGCTCTCAAACTGCGTAAGCTGGAAACGGCTGGATATATCCA
ACAACCAACTCGGGATGCTGACTAACGGGTTTTGATAATCTCTCCACCTGAAAGCAGCTC
ACTGCTGGAAATAACCCCTGGTTTGACTGCACTGAGTATTAAATGGGTACAGAAATGGCTCAA
ATATATCCCTCATCTCTCACAGTGCGGGTTCATGTGCCAAGGTCTGAACAAGTCCGG
GGATGGCGTCAAGGAATTAAATGTAATTTTGTCTGTGCCACCCAGCACCCCGGCTG
CCTCTCTCACCCAGGCTCAACTACAGCTTCTCCGACCATCTAGCCTCCACCTCTCAT
TCAAACCCTAGCAGAAGCTACAGCCTCCAACCTCTACACATCGAAACTTCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGTAACCGGATCCAGCTCTCATC
CATTGGTGAATGATACTTCAGTCAGTGTGCTCTCTCTCACCCTGATGGCATA
CAAACATCATGGTGAAAATGGCCACAGTTAGTAGGGGGCATGTTCAAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACTGAGGCTGTTAACCTAGAGCCCCGATCCACCTATCGGATT
TGTGTTAGTGCCTACTGGATGCTTTAACTACCGCGCGGTAGAAGACCCATTGTTCAAGGC
CACCAACCCATGCGCTCTATCTGAACAAACGGCAGCAACACAGCTCAGCATGAGCAGCA
CGTCCCCAGCATGGGCTCCCCCTTCTGTCGGGGCTGTGATGGGGCGCGGTGATATT
GTGCTGGTGGCTTGCTCAGCGTCTTTGCTGGCATATGCAACAAAAGGGGGCTACACCTC
CCAGAAGTGGAAATAACACGGGGCGGGAAAGATGATTATTGCCAGGGCAGGCACAAAGA
AGGACAACCTCATCTGGAGATGACAGAAACCACTGTTCAAGATGTCCTTAAATAACGAT
CAACTCCCTAAAGGAGATTCAAGACTGCAAGCCATTACACCCAAATGGGGGATTAAATTA
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCACAGCTGGAGC
ACTGCCATACGTGAAGCCAGAGGGCCAGGTTATCAAGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGTCACATAAGACAGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTGCAATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAGTG
CTATTTCTATTCAAGTTAACACAGTTGTAACTCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKSWLIIISLGLYSQVSCKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNQINNAGFPAEHLNVQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDDENSISTVGVEDGAFREAIISLKLFLSKNHLSSPVGLPVLQELR
VIDENRIAVISDMAFQNLTSLERLIVDGNLTLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPP
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQRLMLTQGVFDNLSNLKQILTARN
PWFCDCSICKWVTEWLKYIPSLNVRCFMCGQPEQVRGMARVELNMNLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNSRSYTPPTPTSKLPTIPDWDRGRERVTPPISERIQLSIFHVND
TSIQVSWLSSLFTVMAYKLTWVKMGHSLVGGIVQERIVSCEKQHLSLVNLEPRSTYRICLVP
DAFNYYRAVEDTICSEATTHASYLNGNSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVFLV
LSVFCWHMHKKGRYTSQWKYNRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLKG
DFRLLOPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSGRSISRGRHARTHPTALLESSCENKRADLVII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTTRVGLLQYGSTVKNEFSLTKFKRKSEVERAV
KRMRLSTGTMTGLAIQYALNIAFSEAEGARPLRNVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFIAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRKCGYILNSDQTTCRIQDLCAMEDHNCSEQLCVNPGSFVCQCYSGYA
LAEDGKRCVAWDYCASENHGCEHECVNADGSYLCOCHEGFALNPDEKTCTRINYCALNPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSFGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFAQCQCPEGHVLRSRGDKTCAKLDS CALGDHGCE
HSCVSSEDSFVCQCFCGYILREDGKTCRKDVCQAIHDGCEHICVNSDDSYTCECLEGRPLA
EDGKRCRKKDVCKSTHHGCEHICVNNNGNSYICKCSEGFLAEDGRCKKCTEGPIDLVVID
GSKSLGEENFEVVKQFVTGIDSLTISPKAARVGLLQYSTQVHTEFTLRFNSAKDMKAVA
HMKYMGKGSMTGLALKHMPERSFTQEGARPLSTRVPRAIVFTDGRAQDDVSWEASKAKAN
GITMYAVGVGKAIEEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALEDSGRQDS
PAGELPKTVQQPTESEPEVTINIQDLLSCNSFAVQHRYLFEEEDNLLRSTQKLSHSTKPGSPL
EEKHHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCCGCCAGGGAGGC
CATGATT TCCCGGGGCCCCCTGGTACCAACTTGCTCGGGTTTTGTTCTGGGCTGA
GTGCCCTCGGCCCGGGCCAGCTGCACTGCACTTGCCGCCAACGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGTCTCAGCGTGGTACACCTGACGGGAGGTGCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAAGGAGGATC
AGGTGTTGTCTTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATAAAACCT
TAGAACTCAATGTA
CTGGTCTCCAGCTCCATCTGGCTCTCCAGGGTGTGCC
GTGGGGCAACAGTGACCTGAGCTGCCAGTCTCAAGGAGTAAGCCGCTGTCCAATACCA
GTGGGATCGGAGCTCCATCTTCAGACTTCTTGACCCAGCATTAGATGTCTCCGTG
GGTCTTAAGCCTACCAACCTTCTGCTTCCATGGCTGGAGTCTATGTCAGGCCAC
AATGAGGTGGGACTGCCAATGTAATGACGCTGGAAGTGA
AGCAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGGTACCCCTGGTTGGACTGGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCAACCGCCGGGCAAGGCCCTGGAGGAGGCCAGCAATGATA
TCAGGAGGATGCC
ATTGCTCCCGGACCCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGACCC
TTCCCTGTCACTCCGACAGGCCCTCCGGCACCCCATGGCCCTCCAGGCC
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTACCAAGACTGCCACGACAGAT
GGGGCCACCC
TAACCAATATCCCCATCCCTGGTGGGTTCTCCCTCTGGCTGAGCC
CATGGGTGCTGCGCTGTGATGGTGCCTGCCAGAGTCAGACTGGCTCTCTGGTAT**TGATGAC**
CCCACCACTATTGGCTAAAGGATTGGGGTCTCTCCCTATAAGGGTAC
CTAGCAC
AGAGGCC
TGAGTCATGGAAAGAGTCACACTCTGACCCCTAGTACTCTGCC
CCCC
CTTC
TTTACTGTGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGATTGGAGGAGCCTCCACCCACCCCTGACTCCTCTTATGAAGGCC
CTG
CTGAAATTAGCTACTCAGGAGACTGGCTGGCTGGTCTCTCC
CCCCTGATCTGACCCACCC
TATCTAACACCACCC
CTGGCTCC
ACTCCAGCTCC
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGG
AATCTC
TTATTAAA
ACTAACATGAAATATGTTGTTTCATTTGCA
ATT
AAATAAGATA
CATAA
TGTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEADAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPHPGPPRPGALTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAAPVPMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GMLTQSCGENANCTNTEGSYCCMCPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYVRNSVTDSLPTDIITYIEILAESSSLGYKNNTISAKDTL
NSTLTLTEFVKTVNNFVQRDTVVWDKLSVNHRRTLHKLMTVEQATLRIQSFSQKTTEFDT
NSTDIALKVFFFDSDYNMKHINPHMNMDGYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPNQYDNEEEERVISSVISMSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPGSIGIKDYNILTRITQLG
IIISLICLAI CIFTFWFFSEI QSTRTTIHKNLCCSFLAELVFLVGINTNTNKLFCSSIIAGL
LHYFFLAFAFWMCIEGIHLIVVGVYIYNKGFLHKNFYIIFYGLSPA VVVGFSAA LGYRYYGT
TKWCWLSTENNFIWSFIGPACLIILVNLLA FGVIYK VFRHTAGLKP EVC SFEN IRSCARGA
LALLFLLGTTWIFGVHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

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FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCAAAGNG
AAAAGCCGGCATATGGATTCAATGGCAATGTTGCAGTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTAAACCCACCCAC
ATTATATGAACTGAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTTGGAATACTCACCTGATACCAGAATGGCAGCTGGCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGAAATCACCTGACACA
TTTTGCAATTGATGTCCTGTCCTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTTGCTTGCATATGCATTTACCTTC
TGGTTCTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGTGGCGGTGGGGAGGAGTCCCCGAACCCGGCCG
CTAAGCGAGGCCCTCCTCCCGACATCGAACGGCTGGCGGGGTACCCCGCTGGGA
CAAGAACGCCGCGCCTGCCTGCCCGGGCCGGGGAGGGCTGGGGCTGGGGCGAGGCGG
GGTGTGAGTGGGTGTGCGGGGGGGAGGGCTTGATGCAATCCGATAAGAAATGCTCGGG
TGTCTTGGCACCTACCCGGGGGGCGTAAGCGCTACTATATAAGCTGCCGGCCGGAG
CCGGCGCGCGCTCAGACGAGGCCGTGCGTCAGGATCTAGGGCACGACCATCCAAACCC
GGCACTCACAGCCCCGACGCCATCCCGTCGCCCGCAGCCTCCGACCCCCATGCCGG
AGCTGCGCCGAGAGGCCCCAGGGAGGTGCCATGCGAGGGGTGTGTGGTCCACGTATGG
ATCTGGCCGCCCTCTGGCTGGCGCTGGCCGGCCCGCCCTCGCCCTCGGACGCCGG
CCACGTGCACTACGGCTGGGGGACCCCATCCGCTGGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCACGCTCTCTGCGCATCTCGTGCAGCCGCTCGTGGACTGCGCCGGGGC
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGCTGCTCGGGACCCATCAAGGG
CGTCACAGCGCTGGGTACCTCTCCATGGGCCCGACGCCAGATGCAAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGTTCGAGGAGAGATCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTGGCTCTCCGTGAGCTGGCAACAGCGCCAGCTGTACAAGAA
CAGAGGCTTCTTCACTCTCATTTCTGCCATGCTGCCCATGGTCCCCAGAGGCCCTG
AGGACCTCAGGGGCCATTGGAATCTGACATGATGTTCTCTGCCCTGGAGACCGACAGCATG
GACCCATTGGCTTGACCGGACTGGAGGCCGTGAGGAGTCCAGCTTGAGAAAGTA~~ACT~~
GAGACCATGCCGGGCTCTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTCTACAGAACAGCTCTGAGCTGCCAGCTGTGTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAAGTTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTTGTCTGAT
CATAAACATTCAAGCTGAGCTTGTGCCAGCTGCTGCCCTGGGCCCATCTGCTCCCTGA
GGTTGCTGGACAGCTGCTGCACTGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACTTCTTTGGAAAATTCTTATGTCAGCTGAAATTCTCTAAATTCTCATCACTTC
CCCAAGGAGCAGGCCAGAACAGCAGGAGTAGTTTAAATTTCAGGAACAGGTGATCACTCTGTA
AAACAGCAGGAAATTCTCAACCCCATGTGGGAATTGATCTATCTACTTCCAGGG
ACCATTGCCCCCTCCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGCCAACAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC
CTGAGGGCCAGTTCTGTCATGGATGCTGCTCTGAGAATAACTTGTGCTGCTGGGGGTGTCACCTGC
TTCCATCTCCCAAGGCCACAGGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGCCCT
CCCAAGGCCCCCACCTTATGTCACCTGCACTTCTGTTCAAAATCAGGAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGTGCTGTGGAAAGCAGCGGGGGAGACCTAGAAC
CCTTTCCCCAGCAGTCTTCAATTGATATTATGAGTAATTATTGATATGTAC
TCTCTTATTCTTACATTATTATGCCCAAAATTATATTATGATATGTAAAGTGGAGTTTG
TTTGTATTAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLQYSEEDCAFEET
EIRPDGYNVYRSEKHZLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLES
MFSSPLETDMDPFGLVTLGEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCAGAAGTTCAAGGGCCCCCGGCCCTCGCTCTGCCGCGGGACCTCGACCTCCTCA
GAGCAGCGGCTGCCGCCCCGGAAAGATGGCAGGAGGAGCCGCCACCGCTCCTCTGCTG
CTGCTGCCTACCTGGTGTGCCCTGGCTATCATAAGGCTATGGTTTCTGCCCAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCTGCAAACCCAA
AGAAGACTGTTCTCCAGATTAGAGTGAAGAAACTGGTCGGAGTGCTCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGCGGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAACCTGGAAAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCTCTTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAGA
CAAAGAAGGGATCCAGCTCTGAATACACATGGTTAAGGATGGCATCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGTCATACACAAATGAATAACAAAATGGAACT
CTGCAATTAAACTGTTCCAACCTGGACACTGGAGAATATTCTGTGAAGCCGCAATT
TGTTGGATATCGCAGGTGTCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCGTAGTGTGGCTTAGTGATTTCCGTTGTGGCTTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGACTAATTCTTACATCTAA
ACCCACGACAATGAGTGAATGGCAGTGGCTCACGCCGTAAATCCAGCACTTGGAGG
CCGGCGGGGGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCAATATGGTAAACCC
CATCTCTACTAAAATACAAAATAGCTGGCATGGTCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTAAAAATAAAATAAAATA
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAIACKTPKKTVSSRLE
WKKLGRSVSFVYYQQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TWTLEVVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI
RLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSKATTMSENVQWLTPVIPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

T00170-25820660

FIGURE 25

GACATCGGGAGTGGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAGAG
AAAGAACGAGGAAGATGTGGGCAACATTATTTAACATGCTCCACAGCCCGGACCTTCGGCAT
CATGCTGCTATTCTGCACATGAAAGCAGGGATTAAATTTACTCTTAATAA
ATGAATTACTCAATCTCTGACCATATACATACTCCACCTTCAAAGATCATACTA
TTATATCATTAAGGAAATAGTAACCTCTTCTCCATATGCATGACATTGGACAATG
CAATTGTGCACTGGCACTTATTCTAGGAAGAAAATCTTGTTCTATGGCATTCATCA
TTTGACAATTCAGCAAGCATCTTCTTATACATCAGCTCTTATTGAACTTACTAGCACTGACTG
TGGAACTCTTAAGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CGGAATTCTATGTGCTACTTGGCCTAGCTACACTACAGTACAAGCTGAGATAAAAAG
TGGATTGTCACCGGTTATGTACGTGAAATCAGGCCCTGGTTACACCCAGATCATTAT
ATGGAAGCATCTACATGTGATTGAAATGATTAGCTTGTCTTAACTTCCCAGGACATGGC
AGCTAACACACAGATTCTCTCACAGACTAACAAATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTAATGCGCTGGATTATCTCAAAACAAATTCTACTCGTCACCAAT
ATTATGTAAAAAGATGCCAGCTCCTCTGTGACCTAGGAAAACAAACTTACTGA
ACTGCCCTGAAATCTGTGCTCGAACACTGAGCAACTTACAAGAACTCTATATTAACTACA
ACTGCTTTCTACAATTTCACCTGGAGGCCATTATTGGCCTACATAATTCTCTGACTCTCATCTC
AATTCAAAATGAGTTCAGATGAACTAACAGTAAGTGGTTGATGCTCTTCAAAACTTAGAG
TCTGTAGATGGGGAAAATCTCAATTATCAGATAACAGACATGACCTTCAAGCTTCTTCA
ATCTTCGAGCTGGTTATAGCTGGATAAAACCTCACAGAAATACCAGATAACGCCCTGGTT
GGACTCTTAAAGTAGGAAAGCATCTCTTACGATAACGGCTTAAATAGGATCAACCTGT
TGCTCTTAAAGTAGGAAATCTCAATTCTTGGATCTAAATAAAATCTTAAATAGAGA
TAGCAAGGGGTGATTCTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGTGATAACCTGCCAGATTAAAGAAAATAGAAC
TACTAACACCTCTAGATTGCTTACATTACCCCTAACATTTCTAGACTCCCCAACGCTGG
AACTCATCTGCAACAGCACTGCTCTAGTCCCTGTACCTGTGATTCTGAGCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCATCCCTG
GATGAAACATGAAACAAAACCAATTCTGATTCTGGAGCCAGATTCTGTTGGCTGGACC
CACCTGAATTCTCAAGGTCAAGATGTTGCCCAAGTGTGATTCTGGACATGTTGGAAATTG
CTCCCTTATAGCTCTGAGACTTCTTCTTAATCTAAATGAGAAGCTGGAGCTATGT
TTCCCTTCTAGTGTAGAGCTACTGCGAGAACACAGCTGAAATCTACTGGATAACACCTCTG
GTCAAAAACCTCTGCCTAATACCTGGCAGACAGAACTTGTCTATCTGGAGGAAACACTA
GATATAAACTGGCTGAACTCCAAAAGAAGGGGTTATATACTGTGATAGCAACTAACCTGT
TGGCCTGACTGAAAGTCTGTTATGATAAAGTGGATGGATCTTCCACAAAGATAACATG
GCTCTTGAATTTAAATAAAGATGATGGCAACTTGCAGCTTGTGCTCTGGAAAGCA
AGTCTTAAATCTCAAACTAGTGTAAATGGACAGCTTGTGCTCAAGACTGAAAATCTCA
TGTCTGCGCAAGTGTGCTGAAATCAGGCAACTTGCAGCTTGTGCTCTGGAAAGCA
CATCAACTGAGTAAAAATTGTTGATTGATATCCACCATCTGATCAGAAAACAGAAGAAA
TGTGTAATGTCAACCCAAAGGTTGACCCCTGATCAAAAGAGTGTGAAAGATAATAC
CACAAACACTTGTGGCTGTGGAGCCCTTGTGGGATTATTGTTGTGATATGCTTATCA
GCTGCCCTCTCCAGAAATGAACTGTGATGGTGACACAGCTATGTGAGGAATTAACCTACAG
AAACCAACCTTGTGCAATTGGAGCTTATCTCCCTGTGATAAAATCTCTGGGAAGCAGAAA
AGAAAAGATCAGTAAAGTAAAGAACACTGTGTTAGGTTACCAACAAATATGTCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTOILLLQTNNAKIEYSTDTPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELNSNLQELYINHNLSTISPGAFIGLHNLLRLHLNSNRQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPPLINLRSLVIAGINLTEIPDNAVLGLENLESISFYDNRL
IKVPHVALQKVVNKLFLDLNKPNIRRGDFSNMLHLKELGINNMPELISIDSALVDNLPD
LRKIEATNNPRLSYIHPNAFRFLPKLESMLNSNALSAHYHTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEDPSLFCVDPPEFQGQNVRQVHFRDMMEICLLIAPESFPSNLNV
EAGSYVSFHCRATAEPQEYIWITPSGQKLLPNTLTDKFVHSEGTLDINGVTPKEGGLYTC
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARIPSVDKVYVNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDDGHSYVRNYLQKPTFALGELYPPIN
LWEAGKEKSTSLKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGAATTGCTGACATTCCAGC**ATGAATCT**
GGTAGACCTGTGGTTAACCGTCCCTCTCCATGTGTCTCCTCTACAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCAAGGGCTGTCTTGTTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAATACTAGAGATCTTCCCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCACACTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCCTCAAAAGGAGTAGCTGAAACCTTGCACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCAAAAAATGCCTCAATAACCTGAAGGCAGGGCAGAATTCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCTCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAACTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGGCTGGTCACTATGATCTCATATGTTGATATTATGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAATCCTGCCAAGCAGGCAAAGAAAGCAGATGA
ACCTGATGATATTGACTGTGGTATAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTGCATTGCACTAGAAAATAAGTGGTTACTCTCCCATCCATTGTAACATTGAA
ACCTTGATTTGCACTGTTGATATTGCAACTGCTGAACATTAAACAAACACTACAACA
TAAAATTTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATGAAATTATTTTTT
AATTAAAAGCAAATAAGCTTAACTTGAACCATTGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFLMILCPHSASMC PKGCLSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDQNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLDR
IQSVHKNAFNKLKARARIANNPWHCDCTLQQVLRSMASNHEAHNVICKTSVLDEHAGRPF
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGCCGAGGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCTGCTGGCAGGCCATCTCTGCTGGTGC
GGGCTCAGTGTGTCAGGCTGGCCACGGGCTGCCGCCGCGTGCAGTGCCTCCGCCAGG
ACCGCGCTGTGCTGCCCAGCAGTGCCTTGCGACTGCCAGGCAACGGGATCCCCACCGAG
ACCGCCCTGCTGGACCTAGGCAAGAACCGCATCAAAACCTCAACCAGGACCGAGTTGCCAG
CTTCCCGCACTGGAGGAGCTGGAGCTCAACGAGAACATCGTAGCGCGCTGGAGGCCCG
CTTCACAACACTCTTCACCTCCGGACGCTGGGCTCCCGCAGCAACCGCTGAAGCTCATC
CCGCTAGGCCTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTTCAAGGACTGTACAACTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGGCCCTCAGGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCACATCCCCACCGAGGGCCTGTCACCGCC
CATCGCTCTGGGGCTCCGGCACCTCAACATCAATGCCATCGGGACTACTCTTCAGAGGC
TGTAACCGACTCAAGGCTTGGAGATCTCCACCTGGGCTTACATTGGACACCATGACACCAA
TGCCCTCACGGCTCAACCTGACGTCCCTGTCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCCTCCGACCATCTAGTCTATCTCCGCTTCAACCTCTCCATAACACCCATCA
GCACATTGAGGCTCATGTTGATGAGCTGCTCCGGCTCAGGAGATCTCAGCTGGGG
GGCAGCTGGCGTGGTGGAGCCCTATGCCCTCCGGCCCTCAACTACACTGCGCGTCTCAA
TGCTCTGGCAACCAAGCTGACCAACACTGGAGGAATCAGTCTTCACTCGTGGGCAACCTGG
AGACACTCATCTGGACTCAACCCGCTGGCTGCGACTGTGGCTCCCTGTTGGGTGTCCGG
CGCCGCTGGCGCTCAACTCAACCGCAGCAGGCCACCTGCGCCACCGGAGTTGTCCA
GGCAAGGAGTCAAGGACTCCCTGATGTGACTGCCCACACTACTCACCTGCCCGCG
CCCGCATCCGGGACCGAAGGCCACAGGCTGGTGTGGAGGGCCACACGGTGCAGTT
GTGTCGGCGGGGCGATGGCGACCCCGCCGCCATCTCTGGCTCTCACCCCGAAAGCACCT
GGTCTCAGGCAAGAGCAATGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAAGGTACAGGCAACCGCACCTGCTGCGACTGTGGCCACGCGGGCGGAAACGAC
TCCATGCCGCCACCTGCGCAGCTACTGCCGACTTGCCCCACTGGCCCCATCAGCCAAACAA
GACCTTCGCTTCACTCTCAACAGCGGGGAGGGAGGCGAACAGCACCCGCCACTG
TGCTTTCCCTCGACATCAAGACCTCATCGCCACCCATGGCTCATCTCTTC
CTGGCGTGTGCTCTCTGGCTGGTGTGCTGTTCTCTGGAGCCGGGCAAGGGCAACAC
AAAGCACAAACATCGAGATCGAGTATGCGCCGAAAGTCCGACGCGAGCATCAGCTCCGG
ACCGCCCGCGCAAGTTCAACATCGAGATGATAATGAGGCCGGGGGGGGGGGGAGGGACCCCG
GGCGGCCGGGGAGGGGAAGGGGCCCTGTCGCCACCTGCTACTCTCAGTCTCCCTGCTGCC
CTCCCTACCCCTCTACACAGCTCTTCTCCCTCCCGCTCCCTGCTGCC
CCAGCCCTCACACCGCTGCCCTCTACAGGACCTCAGAAGGCCAGACCTGGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGAGCACCGACCGGGCAAGGTCA
ATAATTCAATAAAAAGTACGAACCTTCTCTGTAACCTGGGTTCAATAATTATGATT
TATGAAAATGAAATAAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCESAQDRAVLCHRKCF
VAVEPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELENENIVSAVEPGAFNNLFNLRTL
GLRSNRKLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVRLRHLNNAIRDYSFKRLYRLKVEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLYVLRFLNLSYNPISTIEGSMIHEL
LRLQEIQLVGGQLAVVPEYAFRGLNYLRVLNVSGNQLTLEESVFHSGNLETLILDNSPLA
CDCRLLWWFRRRWRLNFNRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPAILWLSPRKHLVSAKSNGRLTVFPDGTLLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCCACCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCCTCCCCATCCCCAGCCCCGGGGATT CAGGCTGCCAGCGCCCAGCC
AGGGAGCCGGCCGGGAAGCCG **AT** TGGGGCCCGAGCCGCCAACCTCTCCAGGACGGACAGCCAGCCCTGG
TGTTGCGCTGCTGGCGCCCGGGGCCAACCTCTCCAGGACGGACAGCCAGCCCTGG
ACATCTGATGAAAAGCTGGGTGGCTGGTGGCACCGTGTTGCTCAAGTCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGTCAACCTGCTCAGCAGACTCTACTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCACAGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACTGCTCAATCTTCACTATGCCGT
GCCGAACTGCCAAGTCCCTCGTCACTGTCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGAAC
CTCGAGCCCCGCTCACCTGGAGAAAGGTGACCAAGAACACTCACGGAGAACCAACCCCAT
ACAGGAAGATCCAATGGTAAACCTTCACTGTCTAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTGTGAACCATGAATCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGGGCCAGAAGCTGTGCTCACCTGAGGGTCCGGCAATCAGTCC
CCCGCAGTACCTATGGGAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGGCAGTACAAGGCCTACTACACCCCTAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCAGCCATCATCGTGGGATCGTGGTTCTGTCTCCCTGCTG
CTCATCATGCTCATCTCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAGGCTCCGAGATGCTCCAGCAGCGGACACGGCCATCATCAATGAGAGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTCTAGAGGGCCTGCCACTCCG
GCCCCCAAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCAGCCACCCACCCCTGTACAGAATGCTG
TTTGGGTGCGTTTGACTCGTTGGAAATGGGGAGGGAGGAGGGGGGGGGGGGGGG
TTGCCCTCAGCCCTTCCGTGGCTCTCGCATTGGGTTATTATTATTTGTAACATCC
CAAATCAAATCTGCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLCQVKDHEDSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSPHELSISISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPIPKIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPLKMTQESALIFPFLNKSCTGCTATSNMGSYKA
YYTLNVNDPSVPVSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

03902853-071001

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCCACCCCCCCTTCTCTCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTTGATGTCTGTGGCGACAGGATGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAAATTGCTCGTTAAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGCTCTTTGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAAGGGGACCTACAGCTAGACTGTGAAAAAAGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCAGTTTACCATTTATTCATGCATGCCATT
CCTCACTCGACTTTCCCTAATGAGTTCGTAACCTTTATAATGCGGTTAGTTGACATGG
AAAACAATGGCTTGCATGAAATCGGGGGCTTTCTGGGGCTGCAGCTGGTGAAGAAG
CTGACATCAACAACAAAGATCAAGTCTTCTGAAACGACAGTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTAAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTCGACCATCACCACCTCGACCTCCGGGTAAACAGGCTGAAACGCTGCC
CTATGAGGAGGTTGGAGCAAACTCCCTGTTGCGGAGATCCTGCTAGAGGATAACCCCTT
GGGACTGCACTGTGATCTGCTCTCCCTGAAAGAATGGCTGAAAACATTCCAAGAATGCC
CTGATCGGGCGAGTGGTCTGCGAACGGCCACAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCAGAACAGGACTTGTGCTCTTGGGAAACAGGAGTGGATTCTAGTCTCCGGGCCCTG
CCAAGAAGAGACCTTGTGCTCTGACCCCTGCCAACTCTTCAAGACAAATGGCAAGAG
GATCATGCCAACCCAGGGCTGCTCCAAACGGAGTCAAAGATCCAGGCAACTGCCAGAT
AAAATCAGACCCACAGCGATCGCAGGGTAGCTCCAGGAACAAACCCCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCACTGCGACCCACATCCAGGGTCTGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTGAAAGCCCAAGCTCTAACGTGCGAGGA
GCTTTCTCTCAGAGAACAGAACAGCATCCGCAACTCGGAAATCGCACTTTGTGGTAAACAAGA
ACCTCATTCCTGTTGGATCTGGGCAACATAACATCGCTACTGTAGAGAACAAACACTTCAAG
ACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTGCGGGGCTGCAAACCTAGATGACTCGAACGTTGAGTACAACGCTTACAGCTCA
TCCCTCCCAGGCACTTCAATGCCATGCCAACACTGGAGGATCTCATTCTAACAAACACTG
CTGAGGTCCCCTGCTGGACGTTGCTGGGTCTCCCTCTAACACTCAGCTGCGACAA
CAATTACTTCATGTACCTCCGGTGCAGGGGTGCTGGACAGGTTAACCTCATCCAGA
TAGACCTCCAGGAAACCCCTGGGAGTGTCTCTGACAAATTGCGCTTCAAGCAGTGGCA
GAAGCCTTGGGTTCCGAAGTGTGAGGCGACCTCAAGTGTGAGACCCGGTGAACCTTCTT
TAGAAAGGATTCTAGCTCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTACTTCGCACTGGAGAACAGCACTGGGGAGAACGGGAGCAGCACTCC
AACTCCACTAGACACCCAGGGTGTCCATCTGGTTGCTGGTCTGGACTGCTGTGGT
GTTTGTACCTCCGCCCTCACCGTGTGGCATGCTGTGTTATCTGAGGAACCGAAAGC
GGTCCAAGAGAGCAGAGATGCCAACTCTCCCGTCCGAGATTAATTCCCTACAGACAGTGT
GACTCTTCTACTGGCACAATGGGCTTACAACAGCAGATGGGGCCACAGAGTGTATGACTG
TGGCTCTACTGCTCTCAAGCTAACAGCTAACACCCCAACAGGGAGGGAGAGGG
ATACATCTTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCAAATCCCCCG
CCATCAGCTGGATGGCATAAGTAGATAAAACTGTGAGCTGCACAAACCGAAAGGGCCT
GACCCCTTACTAGCTCCCTCTGAGGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTGTGAGAGGCCCTTTGACAGAAAGCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCTGTGGGGTTGGATGCGCGGGTTCTATAC
ATATATACATATATCCACATCTATAGAGAGATAGATATCTATTCTCCCTGTGATTAG
CCCCCTGATGGCTCCCTGTTGCTACGAGGGATGGCAGTTGACGAAGGCATGAATGTAT
TGTAATAAGTAACCTTGACTTGTGAC

FIGURE 34

MLLWILLLLETSLCFAAGNVTDVCKEKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAFTSQFYH
LFLHGNSLTRLFPNFFANFYNAVSLHMENNGLHIEIVPGAFGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDI DPGAFQDLNKLEV LILNDNLISTLPANVFQYVPITHDLRG
NRLKTLPLYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLDNETTEQDLCPLKNRVDSL PAPPAQETTFAPGPLPTPFKTNGEDHATPGSAPNGGT
I PGNWQIKIRPTAAIATGSSRNKP LANSLPCPGCSDHTPGSLKMCNNRNVSSLADLK
KLSNVQELFLRDNKIH SIRKSHFVDYKNL ILLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQLQNLEYLNVEYNAIQLILP GTFNAMPKLRIL LILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQ LTSII QIDLHGNPWECSCTIVP F KQWAERLGSEVLMSDLKC
ETPVNFFRKDFM LLSNDE ICPQLYARISPTLTSHSKNSTG LAETGTHSNSYLDTSRV SISVL
VPGLLL V FV TS AFTVV GMLV FIL RNRKRS KRR DANSSASE INSLQTV CDSSYWHNGPYNADG
AHRVYDCGS HSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

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FIGURE 35

AGTCGACTGCGCCCCGTGACCCGGCGCCAGCTGTGTTCTGACCCCAAGAATAACTCAGGGC
TGCACCGGGCCCTGGCAGCGCTCCGCACACATTCTGTCGCCGCTAAAGGAAACTGTTGCC
CGCTGGGCCCCGGGGGGATCTTGGCAGTTGGGGGGTCCGTCGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGGCTCTCGAGCGGGAGAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG
AGAATGAGGCCGGCTTCGCCCTGTGCCCTCTGGCAGGGCCTCTGGCCCGGGCGGGCG
CGGGCAACACCCACTGCCGACCGTGTGCTGCCGCTCGGGCTCGGCTACAGCGCTGC
ACCAAGCTTACCATGAAGCGGGCAGGGGGCAGGAGGGCTGCATCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGGGGCGCCAGCTGCCGCTGTGCTCGCCTCTGCGGGCAGGCCCCAGG
GCCCGGAGGGGCTCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTCCCAC
GCACCCCTGGAGAACGAGCTTGCCTGGGGGTTCTCTGGCTGTCTCCGACCCCGCGGTCTC
GAAAGCGCACCGTGTGAGTGGGGAGGAGCCCCAACGCTCTGCACCCGCGAGATGCGC
GGTACTCCAGGGCACCGGGTGGCTGAGCCCCAGGCTGGAAGGAGATGCGATGCCACCTGC
GGCACAAGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGCTGCTGCCGCGCCCCGG
GCCGCCCTTAACCTGAGCTATGCCGCCCTTCAGCTGCCACAGGCCGCTCTGGAGATTCA
TCCACCTGGGACCGAGGTGAGTGTGCTGCCGCTGCCGGGGCACAGCTCCGATCTCAGTTACTGCA
TCGGGGCAAATCGCGCTCGTGGGACAAACTCTGGGCATGTGTTGTCCTGCC
GGAGGTACCTCCGCTGGCAAATGCGCAGAGCTCCCTAATGCCCTAGACGACTTGGGAG
CTTGCCCTGCCAATGTCATGGGCTTCAGCTGGGGAGGAGCAGGCCCTTTGTCGACCA
GTGGGGAAAGCACAGGCCACCTGGGGGACGGGGTGGGACCCAGGCCGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGCCAATCAGGGTGACGAGAAGCTGGGAGAGAC
ACCAACTGTCTGCAAAAGACAATTCAAGTAACTCATCTTCTGAGATTCCTCGAGATTC
CACAGAGCACAGTGTCTACCTTCAAATGTCTTCAAGGGCAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGTCTTCAAAGTAACTCACGACTTCTCTGCCACTCCTCAGGCTTT
CGACTCCCTCTGCCGTGGTCTTCATATTGTCAGCAGCAGTAGTGTGTTGGTGTATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTCAAGGAAAGGCCCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCCGGGGCTGGAGAGTGTCTGAGGCCGCTGCTTGGGCTC
CAGTTCTGCACATTGCACAAACAATGGGGTGAAGAGTCGGGACTGTGATCTGCCGGACAGAG
CAGAGGGTGCCTTGTGCGGGAGTCCCTCTGGCTCTAGTGTGATGCATAGGAAACAGGGGA
CATGGGCACTCTGTGACAGTTTCACTTTGATGAAACGGGGAACCAAGAGAACATTAC
TTGTGTAACTGACAATTCTGCAAGAAATCCCCCTCTCAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCTTCCCTGATGATGAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTGAACTGGGGACGGGGTAGTGTGGGGAGAGATTTCTTATGTTATTGGAGAA
TTGGAGAGTGTGAACTTTCAAGACATTGAAAGGAATAGAACACAATATAATTACA
TTAAAAAAATAATTCTACCAAAATGGAAAGGAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCAGGGAAAAAAATAAAAATAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGGPGGEHPTADRAGCSASGACYSLHHATMKRQAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGSKDLFWVLAERRSRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVVEPQRSCSTARCAVLQATGGVEPAGWKMCRHLRANGLYLKQFVEVLCAPRGA
ASNLSYRAPFLQHSAALDFSPPGTEVSALCRGQLPISVTCTIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLLGGFACECATGFELKGDKGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPVQRTWPIRVDEKLGLETLPVEPQDNDSVTSIPEIPRPGSQTSTMQLSMSQAEKATITP
SGSVISKFNSTTSSATPQAFSDSSAVVFIVFVSTAVVVLVILTMVTLVGLVKLCFHESPSQPR
KESMGPPGLESDFPFAALGSSAHACTNNVGKVGCDDLRLDRAEGALLAEASPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACCGCTGGGATTCAAGCATGGCTGGCTGCCAGAGCAGCTCTAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATACTGCCTTAAAAGTGCCTCCGCCCTGCCGGCGCGTATC
CCCCGGCTACCTGGGCGCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGGCAGCCGA
GGCCCGGTGTGAGCCACGGCTGCCAGTGTGAGCGGGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGCGCGCGCGCGCGTGGGTGCAAAACCCCGAGCGCTACGCTGCC**ATGA**
GGGGCGCGAACGCCCTGGCGCCAECTCTGCCCTGCTGCCGCCCCAGCTCTCGCG
CAGCAGTCCCCAGAGACCGTGTGTTACATGTGCTGCCATTCTTAAGTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGACCCCTCAAATAGCAAAATGTACTTGGAAAATCA
CAGTTCGGAAAGGAAAGTAGTCGTTCTCAATTTCGATTATAGACCTCGAGAGTGAACAC
CTGTGCCGTATGACTTGTGGATGTGTACAATGGCCATGCCAATGGCAGCGCATTGGCCG
CTTCGTGCCACTTCCGGCTGGAGCCCTTGCTCCAGTGGCAAAAGATGATGGTGCAGA
TGATTCTGTGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCCGCTGTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCTTGACAGACCTCCGGCTTTAAC
CCCCAACTGGCAGACCGGATTACCTCGAGGAGTCACTTGTGTGTCACATTAGCCC
AAAGAAATCAGCTTATAGAATTAAAGTTGAGATGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCACAGTGTAGAAGATTGGAAA
GTATTGTGGTGTAGTCCACCTCGCCAATTGTGTCAGAGAGAAATGAACTTCTTATTCACT
TTTTATCAGACTTAAGTTAACTGCAGATGGTTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCCTACAACAGACAGCTGTCACCACACCTCTGTAACCACGGGTTAAA
ACCCACCGTGGCTTGTGTCACAAAAGTAGACGGACGGGACTCTGGAGGCCATTATT
GTCAAGTGACTTGTGTTAATGGCCGCACTGTATCACACCATCACTCCGATGGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTAACAGGGAAATTGGCGATTCAAGCAGCGGG
CAAGAACATGAGTGCAGGCTGACTGTGCTGCAAGCAGTGCCTCTCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAGATGGCGAGGCAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAAGCTCTGGATGCCCTTAAAAAAAGCAATG
TAAACAGTGAACTGTGCTTAAAGCTGTATTCTGCCATTGCAATTGGCTTGAAGAGTCTATGTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGITGACTCTCACATGATGGAGGTATGAGGCCCTCGAGATAGCTGAGGGAAAGTTCT
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAAACCTGCCGACTTAACTGCGGGTGTAGGA
AGCTAAAGTAGTCAGCGTTGACAGCTGGAAAGCGTTTATTATCATCTGTAAAGGAGT
ATTTAGAATTGAGTTGTGTAAGATGTCAAAAAAAGATTTTAGAAGTGTCAATTATGTTAGT
GTTATTGTTTACCTTCAAGCCTTGCCTGAGGTGTACAATCTTGTCTTGCGTTTCTA
AACTCAATGCTTAAATAAAATTTTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPRDYPAGVTCVWHIV
APKNQLIELKFKEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSSLTADGFIGHYIFRPKKLPTTEQPVTTFPVTTLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTTTRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMQVGVEDGRGKIMPNSFIMMFKTKNQKL DALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACCGTGGCGGCCACGGCGCCCGGGCTGGGGCGTCGCTTCTT
CCTTCTCGTGGCCTACGAGGGTCCCAGCCTGGGTAAAGATGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTTCTCACACCTCCCAGGACCTATCTGG
CTCCAGGCCCTCCACCTCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCCTGGAGAGAACCATCCGGACAACCTTGGAG
GTGGAAACACTGCCCTGGGAGGAAGAGAATTGTCCAATACAAAGACAGTGA
GAGCACCGAGGGGCTGGGAGGAGCTGGTGGTTCAAAAGCAGCAGGAGGGCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC
CTTCCCTGTCTGGGGAAACAGAGAGGCCCTGCGGTGGCTACGGGAGTGTGAAGGAGAAGG
GACACGAGGGGCAAGCGGGACTGTGACTGCCAAGCCGCTACGGGGTGAGGCCCTGGCC
AGTGTGGCTTGGCTACTTGAGGAGAACGCAACGCCACGCCATCTGGTATGTTGGCTTGT
TTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCA
ACTGTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCAGGTCGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGGGGCTCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCGGAGAGA
ACAAGCAGTGTAAAACACCAGGGCGTTATCGCTGCATCTGTGCCAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAAGCAGATGTTGGCATCATCTGTGCACTGGCA
CGCTGGCTGCTAAGGGCGACTTGGTGTCAACGCCATCTCATTGGGCTGTGCCAGGCCATG
ACTGGCTACTGGTTGTCAAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGAGATA
ATCGCGGCCACCCACTGTAGGACCTCCCTCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTTAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCTCACAGGGTGGGGCCATCACAGCTCCCTCTGCCAGCTGCATGCTGCCAGTCTCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATCATCAGGAAATAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAA

FIGURE 40

MAPWPPKGGLVPAVLWGLSLFLNLPGPWIWLQPSPPPQQSSPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEEEENLSKYKDSETRLVEVLEGVC SKSDFCHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLP CGGTERPCGGYGC QCEGEGRGGSGHCD CQAG
YGG EACGQCG GLGY FEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVD IDE
CGT EGANC GADQFCVNTEG S YECRDCAKA CLGCMGAGPGRCKKCSPGYQ QVGSKCLDVDE CE
TEVCPGENQ CEN TEGGYRCICAEGYKQMEGICVKEQI PESAGFFSEMTEDELVVLQQMFFG
IIICALATLA AKGDLVFTAIFIGAVAAMTGYWL SERSDRVLEGFI KGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCTGCAGCCTTCAAGGGACAGCCCCACTCTGCCCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCCTGGCAGGCCAGCTGCGGAGCTCAAAAGAGGT
GCCCACCCCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCCCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGCG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGAGGCCGTGCTGCCGCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGACAGGGCGGTGCTCCCGCGCAGGCCCGGGC
CGGGTGACCGCTGAGTGGCTGCGCGTCCAGGACAGGGCTTACAGGTGACCGAGGGCGTGA
CTCCAGGCTGGTGTCCCGTCCAGGAGAGCGCTGGAAAGGCCAGTGCTACAGGTGCGAGAGG
ACTTCTGGCAGCAGCTGAGCGGCCCGGAGCGCGTCTGCTACAGGTGCGAGAGG
GAGCATCTGGGCCGCTGGCGCCGCCACAAGCTGGTCCCGCTTGCTCGCAGGGGGC
GCCAGCCGGGCTGGGAGGCCAGCTGGAGCTGCACACCCCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGCCCCCGGCTT
CCTGGCTTATGAGTGTGTTGGCACCTGCCAGCCCCGGAGGCCCTGGCCTTAAGTGGC
CGTTCTGGGCCCTGACAGTGCATGCCCTGGAGACTGACTCGCTGCCATGATGGCAGC
ATCAAGGAGGGAGGCAGGACCAAGGCCAGGTGGTCAGGCTGCCAACATGAGGGTGAGAA
GTGCAGCTGTGCCCTGGATGGCGCTCGTAAGGAGGCTCAGCCATGGCGCCTAGTG
TAGGCATCGAGGGACTTGACTTGTGTTCTGAAGTGTGAGGGTACAGGAGAGCTG
GGATGACTGAACCTGCTGATGGACAAATGCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTTGCTTCTCAGGAATGAGAAATCTTGCCACTGGA
GAGGCCCTTGCTCAGTTCTTCTATTCTTATTACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCCCTGTAC
TGGATCTGGCTAAAGTCCTCACCACACTGGACCTAACGACTGGGGTTAAGTGTGGGT
TGTGCATCCCCATCCAGATAAAAGACTTGTAAAAACATGAATAAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSSLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRQLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

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FIGURE 43

GTCTGTTCCCAGGAGTCCTCGCCGGCTGTTGTCACTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCCTTCATATTGGCATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACTCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTGTCTGTGCCACTCGGGCTTTCTCTCCCCGTGTGGAGTGGAAAGTTGACCA
AGGAGACACCCAGACACTGTTGTATAATAACAAGATCACAGCTTCTATGAGGACCGGG
TGACCTTCTTGCCTACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGATGGTCTGTAGGAAAGCGGCAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCCATCCAAGCCTACAGTTAACATCCCCCTCTGCCACATTGGGACCGGG
CAGTGTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT
GGGATAGTGTGCTACGAATCCCCAAAGCACCGTGCCTCAGCAACTCTTCTATGTCCT
GAATCCCCAACAGGAGAGCTGGCTTGATCCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGATGGAAAGCT
GTGGAGCGGAATGTGGGGTACATGTCAGCCGTCCTGTAAACCCGTATTCTCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCATAGCCGAGGCCACTTGACAGAACAAAGAACGGGA
CTTCGAGTAAGAAGGTATTACAGCCAGCTAGTGGCCAGTGAAGGAGAATTCAAACAG
ACCTCGTCACTCCCTGGTGTGAGCTGGTCCGCCTACCCGCTATCATCTGCATGGCCTTACT
CAGGTGTACCGGACTCTGGCCCTGATGTCTGTAGTTACAGGATGCCATTGGTCTTC
TACACCCACAGGGCCCCCTACTCTTCGATGTGTTTAATAATGTCAGCTATGTGCCCC
ATCCTCCTCATGCCCTCCCTCCCTTCTACCACGTGCTGAGTGGCCTGGAAACTGTTAAA
GTGTTTATCCCCATTCCTTGAGGGATCAGGAAGGAATCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGGGGGTGCAGGAATCTGCACTCAACTGCCACTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTTCTGGCCTCTTCTTGACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGGCTTCCATCTGGGCCACTCTCTGTCTTCCATGGAAAGTG
CCACTGGGATCCCTCTGCCCTGTCCTCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGAGAGGCTAGTAAATTTCAGAGAACCTGAAGC^{AAA}AG
GATTAAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGGCGCAGTGGCTCACGCC
TAATCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGGAGTTGGGATCAGCCTGACCA
ACATGGAGAACCCACTGGAAATACAAAGTTAGCCAGGATGGTGGTGCATGCCGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGAAAACTCCAGCTCAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGN SYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGI VMPTNPKSTRAFSNS
SYVLNPTTGEELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVG VIVA AAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEG EFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCGCTGTGGGACAGCATGAGCCGCGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCAGTCGCGCACAGTGGCTATGCGTGCCTCACCTGG
CGCTCGACAGGGACTTGGACTGCAGCGATGGCAGCAGTGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCGCCTGGCTGCCTAGCA
GGCGAGCTCCGTTGACGCTGAGCGATGACTGCATTCACTCACGTGGCGTGCAGCGCA
CCCGAAGTGTCCCAGCTCAGCGAGCGTGGAGACCATGAGATCCTCCCGAAG
GGGATGCCACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAAC TGCTATGGGTTATTGCA GCTGCTGCCGTGC
TCAGTGCAAGCCTGGT CACCGCCACCCCTCCTCCTTGTCTGGCTCCAGGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAC
CTCGCTGCCTGAGGACAAGCAACTTGCACCACCGTCACTCACGCCCTGGCGTAGCCGACA
GGAGGAGAGCAGTGTGCGGATGGGTACCCGGGACACCCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCTGCAAGAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

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FIGURE 46

MSGGWMAQVGAWRTGALGLLLLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNCSRLA克莱LRTLSDDCIPLTWRCDGHPDCPDSSDELCGGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPVGNAATSSAGDQSGSPTAYGVIAAAAVLSASLVATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCCACGCGTCCGGCTCGCTCGCAGCGCGGGCAGCAGAGGTGCGCACAGATCGGG
GTTAGACTGGCGGGGGGGAGGAGGCGGAGGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATCATGGAATGACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCACGAGCACACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGCGGGT
CGATGACCTTCAGTGTGCTGACCCCGCATTCCCGAGAATGGCTTCAGGACCCCAGCG
GAGGGGTTTCTTGAAAGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAGAGACTGTGTTGAAGCATTAACTGGAACCTAGGCTGGATCCAAGTG
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATA
ACAAGACATATAGACATGGAGAGAACGCTAATCATCACTTGTCTGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCAATTGTGCGCATGATGGAACGTTGAAATACTG
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTTCTAATGGCTATGTAACATCTGTG
TCCAGACCTCTTCCGGGGGGACTGTGATCTCCTATCGCTGCTTCCCGATTAAACTT
GATGGGTCTGCTATCTTGAGTGCTTACAAAACCTTATCTGGTCTGCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCAATGGTAGTCAAGGAGATTCTG
GCCACCCGGCGCTGTGAGCGCTACAACCACGGAACTGTGGTGGAGTTTACTGCGATCTC
GGCTACAGCCTCACAGCAGTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCTTC
TTATCAAGTCACTGCTACAATCAGAGCAACGTTGCCCCAGCACCATGAGACCCCTCTGA
CCACGTGGAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGCTGCTGCTGCTCATC
CTGGCCAGGATGTTCCAGACCAAGTCAAGGCCACTTCCCCCAGGGGCTCCCGGAG
TTCCAGCAGTGAACCTGACTTGTGGTGGTAGACGGCGTCCCGTCATGCTCCGCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCCGGTACATGGCTCTGGCCAG
GGCTGCCCTTACCCGTGACGACCAAGAGCCCCCAGCATACCCGGCTCAGGGGACACGG
CACAGGCCAGGGAGTCAGAACCTGTGACAGCGTCTCAGGCTTCTGAGCTGCTCCAAA
GTCTGTATTCAACCTCCAGGTGCAAGAGAGCACCCACCTGCTGGACAAACCTGACATA
ATTGCCAGACGGCAGAGGAGGTGGCATCCACCAAGCCAGGATCCATGCCCCACTGGG
GTTGTTCTAAGAAACTGATTGATTTAAAAAATTCACCAAGTGTCTGAAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTCTGGTTAGACAAATGTAACAA
AGCTCTGATCTTAAATGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTCTTCTGACACAGACTGATTTAAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLBQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKGTAKRLCLKHFNGLTGWIPLSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMSLCRDDGTWNNLPIQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEVAESTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FOOT 25320690

FIGURE 49

CCACCGCGTCCGCTCCGCCCTCCCCCGCTCCGTGCGGTCCGTCGGCTAGAGA
TGCTGCTGCCGCCGGTTGCAGTTGCGCAGCCTCTGCCGCCAGCCGCTCACCG
AGCGCCCGAGTGTGGGGGGCGCACCGAGTCGGGCCATGAGGCGGGAAACCGCGTACAGG
CCGTGCTGCTGCCGTGCTGGTGGGCTGCCGCCAGGGCTGCTGAGTGC
TCGGATTGGACCTCAGAGGAGGGCAGCAGTCTGCCGGGAGGGACAGAGGCTGTTA
TAAAGTCATTTACTTCATGATACTCTCGAAGACTGAACATTGAGGAAGCCAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCAGAAGATGAACAGAAACTGATAGAA
AAGTTCATGAAAACCTCTGCCATCTGTGGTGACTCTGGATTGGCTCAGGAGGCGTGA
GGAGAAAACAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGACTGATGGCAGCATAT
CACAAITTAGGAACTGGTATGGATGAGCCGCTCTGCCAGCGAGGCTGCGTGGTCA
TACCATCAGCCATCGCACCGCTGGCATCGAGGCCCTACATGTTCCAGTGAATGATGA
CCGGTGCAACATGAAGAACATTTCAATTGCAAATATTCTGATGAGAACACAGCAGTCC
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCCTGAATCTGCC
CCTAATCCCAGCATTCCCTCTCTCTCTGTGGTACCACTGTATCTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTCTAGCACAAGAGCAACACACC
TGGCCCTCTCTCACAGGGAAACAGCCGGACTAGAGGTCTACAATGTCATAAGAAA
AAAGCAGACTTAGCTGAGACCCGGCAGACCTGAAGAATATTCAATTCCAGTGT
CGGGAGAAGCCACTCCGATGACATGTTGTGACTATGACAACATGGCTGTGAACCC
GAAAGTGGTTGTGACTCTGGTGGAGCTAGAGGTCTGGATGGTGGAAATGAA
GTTCTCCCCAGACCAAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAATGAA
GTTATTAGGACATATAAAACTGAAACTGACAACAATGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAAATACACAGAAGGTCTATGAAACAGCTTAGATCAGG
GGATGAGCATGTGGTCCCCACGACCTCTGGACCCCCACGTTGGCTGTATC
CCCAGCCAGTCATCCAGCTGACCTTATGAGAAGGTACCTTGCCAGGCTGG
GAGTCTCAATAATGTCATTGGTGGTTGATCTAACTTTAAGGGACAGAGCTTAC
GCAGTGATAAAAGATGGGCTGAGCTGGAGAACCCACCTCTGTTCTGCT
CAGCACATATTATCATAAGACAGAAAATCCAGAACATCTTCAAGGCC
GTTGGCCTGTGCATCGCAATTCTCATATGTTTTCAAGAAATAAAATCAA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIEKFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPETQEEDAKKTFKESREAALNAYILIPSIPLLLLVL
VTTVVVCWWICRKRKREQPDPSSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVESGFVTNDIYEFSQPDQMGRSKES
GVVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCGGGAGGCACAGCGGTCCCTGTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCGCAGAAGACTTGT
GTTGCCTCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCATGATCACTGGTGT
GTCAGCATGCCCTGTTGAGCCCGATGGCGTCTGACCTCGCTGGCGTACTGCCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTGCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTGACACGGGGCTGGAGTCCTCTCAAGCC
GCTCCCCTGGAGGAGCAGGTAGACTGGAACCCCCAGCTATTAGAGGTCACCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTATTGCTTCAACTAACATTTCGGAATCTG
GAGTCCACCCGGTGTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAGACTCTGTATCCCAACTACCAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTAAAGTGGACTTCTCATCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCTAGAGAGAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAAATAAGGCCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYVTNLAGGPKPYSFYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFIILLDNVAAEQAHLNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCP LDMLFLNAMS VYTLSPEKYHALCSQTQVM EVGN EEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCCTTAACATACTTGAGCTAAA
ACTAAATTTGCTGCTTGGGACCTCCTCTAGCCT
TAAATTTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCGCTATTCTCCTGATCCTT
GCCATTGACAGACCTGGATTCTAGCGCTCCATCTGGAGTGCGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGTGGAGGTGGAACAGAAAGGCAGTGGGACCGTGTGATG
ACGGCTGGACATTAAGGACGTGGCTGTGGTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTGTGAGGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAAGATTATG
ATTGTTACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCAAGCTGGCTGACGCCCTGGGATGTGCAAGGGACGCGTGGAAAGTGA
GCACCAAGAACCGTAGGTGATACCGTGTGCCAGACAGGCTGGACGCCCTGGGCGCAAAGGTGG
TGTGCCGAGCTGGGATGTGGAGGGCTGTACTGACTCAAAACCTGCAACAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCAGTCAAGGACGAGAACCTTCA
GGATTGCCCTCTGGGCTTGGGAGAACACCTGCAACCATGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCTATGGGCTCTGCTGTGATGACAACCTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAGTCCTCTCCCTCTGAGACCCGGA
AATGCTATGCCCTGGGTTGGCGCATCTGGCTGGATAATGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCACAGATTTGGGGTTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCAGTCACTGCTCAGTGGCATCTAATCTGTTGAGTGCCTGAATAGAA
AAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGGACTTAACTTGTGCCCTGATTCAGGCCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATGTTGAACTACATCA
CCACCTTCTATGTCCTCACATTGACACAGCAGATTCCAGCCTCCATAATTGTGTTGAT
CAACTACTTAAATAACATTCACACACACACACACACACACACACACACACACATA
CACCATTTGCTCTGGTAAAGGATAAAATTCTGAAGAACCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAAATTAAAGGATAAAATTCTGAATTGGTTATGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTACATAAAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFLSLILAICTRPGLASPSGVRLLVGGLHRCEGRVEVEQKGQNGTVDDGWDIKDVAVL
RELGCAGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEELYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGRCKGRVEVKHQHQWYTCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQLMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCGSRLEVHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

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FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGGGACCGTGGCGGACCGTGGGCCGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGACTTCATCACCTCCACAGGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGCTTCGGCCTCTTCGGCTGCTGCAGTGGGCGCGGAAAGGCCACCTGCCGAATGCTG
TGGTGGTGATCACAGGGGCCACCTCAGGGCTGGGAAAGAATGTGCAAAGTCTTCTATGCT
GCCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAAGAGCTCATCAGAGA
ACCTTACCGCTTCTCATGCCACCAAGGTGCAAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGG
TGTGGACAAGGGTCAAGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGAAGGCCACATTGTCGCCATCAGCAGCATTGGCAAG
ATGAGCATTCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGCGGAGATGGAACAGTATGAAATTGAGGTGACCGTACAGCCCCGGTACA
TCCACACCAACCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCAACACAGCCCAGGGCGAAGGCCCTGGAGGTGGCCAGGATGTTCTGCTCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCTTGGCTGTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCAGCCTCATGGCCTCCAGGGCAGAAAAGAGCGAAATCC
AAGAACTCCTAGACTCTGACCAAGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGTCTCACAAGTGGG
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAACGACAACA
AGCTTCTCCCAGGGTGAGGGGAAACACTTAAGGAATAATATGGAGCTGGGTTAACACT
AAAAAACTAGAAATAAAACATCTCAACAGTAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAACGCTGGCCCATGGCCAATTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSLGKEAKVFYAA
KLVLCGRNNGGALEELIRELTASHATKVQTHKPVLVTFDLTDGAI
VNNAGISYRGTIMDTTVDVKRVMETNYFGPVALTKALLPSMIKRQQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVVAQDVLAvgKKKDVLADLLPSLAVLRTLAPGLFFSLMASRARKERKSNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

00070-07100-05820560

FIGURE 57

CCACCGCGTCGCTGGTGTAGATCGAGCAACCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAAACACACAAACGCTCGCAGCCACAAAGGGATGAAAATTCTCTGGACATCCTC
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGACTCCCTGTGAAGCTTTTATCCCTAA
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GACTGACTGCCATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTG
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAA
GGCATTTCCTCTGCAATGACGAAGAAACCATGGCATATTGTCAGTGGCTTGGCAG
CTGGACATGTCCTGGTCCCCCTTACTGGCTTACTGTTCAAGCAAGTTGCTGTTGGA
TTTCATAAAACTTTGACAGATGAACGGCTGCCTTACAATAACTGGAGTCAAAACACATG
TCTGTGTCCTAATTCTGAAACACTGGCTTACTGTTCAAGTACAAGTTGGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGTGATGCACTGGATTCTGACTGAGCAGAAAGATG
ATTTTATTCCATCTTCTATAGTTTAAACACATTGGAAAGGATCCTTGTGAGCGTTT
CTGGCAGTTTAAACGAAAATCAGTGTAAAGTTGATGCAAGTTGATGTTGGAATAAAATGA
AAGCGCATAAGCACCTAGTTCTGAAAACACTGATTTACAGGTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTAAATGTTGAACCTCTGTTTTCTAATTATCCCATTCTCAATA
TCATTTGAGGCTTGGCAGTCTTACCACTGTTCTTAGCCAAAGCTGATT
ACATATGATATAACGAGAAAATACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTATTAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
AATTGTACCATACCGTTATTAAACATATAATTTTATTGATGCACTTAAATTGTT
ATAATTGTGTTCTTCTGTTCTACATAAAATCAGAACTCAAGCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTCAATGAATATCATGAACTCTCAATGGTAGGTT
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCCAATGCCAAACATTCT
GCACAGGGAAAGCTAGAGGTGGATACACGTGTTGCAAGTAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 58

MKFLLDILLLLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

1000-0710032-2858200501

FIGURE 59

CCACCGCTCCGGACGGCTGGGTCGACTAGTCTAGATCGCGAGGGCCGCCGGCTC
AGGGAGGAGCACCGACTCGCCGCACCCCTGAGAGAGATGGTTGTGCCATGGAAGGTGATTG
TTTCGCTGGCTCTGTGATGCCCTGGCCCTGTGATGGGTGTTCGCTCCCTATAAGAAGT
GTTTCATGCCACCTAAGGGAGACTCAGGACAGCATTATTCTCACCCCTTACATTGAAGC
TGGGAAGAGTCAAAAAGGAAGAGAAATTGAGCTTGTGGAACATGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGCTTCTCAGCTGAATAAGACTTACAACAGCAACCTCTTCTGTT
TTCCCAGCTCAGATACAGCCAGAACGATGCCCTAGTAGTCTCTGGCTACAGGGTGGCCGG
AGGTTCATCCATGCCAGAGACTCTTGTGGAACATGGCCCTTCCCAGGACTGAACATGA
CCTTGCGTGCAGAGACTCTCCCTGGACACCAACGCTCTCATGCTTACATTGACAATCCA
GTGGCACAGCTCAGTTACTGATGATACCCACGGATGAGCTCAATGAGGACGATGT
AGCACGGGATTATAACAGTCCACTAATTCACTAGTTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAAGGAAATATGTCAGGCCATTGACACCTC
ATTCATTCCCTCAACCCCTGTGAGAGGTAAGATCAACCTGAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGCTATGAGAAATTCTGTACCAAATTGGCT
TGTGGATGAGAAGCAAAAAGACTTCCAGAACGCTGCAATGAGAACACATC
AGGAAGCAGAACACTGGTTGGGCTTGAATACTGGATAAAACTACTAGATGGCCTAAC
AAGTGATCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTCCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTAAGGAAATTGGTCACTCCAGAGGGAGACAA
GCCATCCACGTGGGAATCAGACTTTAAATGTTGAAACTATGTTGAAAAGTACTTGGCGAGA
AGATACAGTACAGTCAAGTAAAGCATGAAATCATGAAATTATAAGGTTCTGA
TCTACAATGCCAAGTGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTTGTGGC
ATGGACTGAAAGGATCCCGAAATACAAGAAGGAGGAGAAAAAAAAGTTGGAAGGATTTAA
ATCTGACAGTGAAGTGGCTGTTACATCCCGCAAGCGGGTGACTIONCCATCAGGTAATTATT
GAGGTGGAGGACATAATTACCCCTATGACAGCAGCTCTGAGAGCTTGTACATGATTAATCGA
TTCATTTATGAAAAGGATGGATCCTTATGTTGATAAAACTACCTTCCAAAAGAGAACAT
CAGAGGTTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATTAAAAAA
TTATCTTTCATATCTGAAAGATTTTCTCATAAATAAAATTATCCTTGAACAACTGAGC
TTTGTGTTGGGGGAGATTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGATGATGTCAGACTGAGACAAGATGTTAAATG
AATTGGTGGCTTGAATAGGAAGTTTAATTCTTAAGAGTAAGTAAAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCAATAACAGAAGTTGGCATGCCGTGAAAGGT
GTTTGGAAATTATTGATAAGAATAGCTCAATTATCCAATAATGGATGAAAGCTAA
TAGTTTGGGAAAAGATTCTCAAAATGTTAGAACAAAAGAATTCTTGAATA
AAATATTATATAAAAGTAAAAAAAAAA

FIGURE 60

MVGAMWKVIVSLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL
S
VGPFPGLNMKSYAGFLTVNKTYNSNLFFWWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
G
GPYVVTSNMTLDRDFPWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEEDDVARDLYSALIQF
P
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLNPKREVKINLNGIAIGDGYSDPESIIGG
Y
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLDGLTSDPSYFQNVTG
C
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
E
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEEKKVWKIFKSDSEVAGYIRQ
A
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

09902053 - 010170

FIGURE 61

CGAGGGCTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCCTGTTGGCTAACACAT
TTTCCTTCTTAAACAATCTAACAGCTTCAACAGCTAGTGATCAGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTACCGAGCTCTG
CCTCTGTGATAACAGACATGAGAAAGTGAAGAGATGAGCAGGGAGGTGAGGTGATGGAAG
TCTAAATAGGAAGGAATTITGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCCTAACAAAGCTTCAAAAAACAGGAGCAGTCCACTGGCTGGGAT
AAAGACGTGCCGGTAGGATAGGGAAAGACTGGGTTAGTCTAAATATCAAATTGACTGGCTGGG
TGAACCTTCAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGTTGTAATAAATTTAAAAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATCCCTAACATCTTCAAGAGGGAGAAAGTATGTTAAAGGCTAGA
GAAAAACCAAAATGCAGAGGGAGACTCACAGAGCTAACACCAGGATGGGACCCCTGGGTC
AGGCCAGCCTTGTCTCCGGAAATTATTTGGCTGACCAACTCTGGCTTGTGTTT
GCAGAACATGTAGGGCCAACCGGGGAAGGGTGGAGCAGAGTGAACACAGGAGCCCT
CCTCACCGCCGCCCTCTAGCATGGAACAGAGGAGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCGCTCTGGCTCTAGTGGCTGCTGGCTGCTGGCCCCCAGCAGGCC
ATGCCCTAGTCAGCACCTTCACTTGAGAATCGTACGGACCTTCACCCACTTGACCGT
CCACCAAGGGACGGGGGGCGCTATGTGGGGCCATCAACCGGGCTTAAAGCTGACAGGCA
ACCTGACCATCACGGTGGCTATAAGACAGGGCCAGAAGAGGAAACAAAGTCTCGTACCCG
CCCTCATCGTCAGCCCTGAGCTGGCTCACCCTCACCAAAATGTCACAAACAGTGT
CATCATTGACTACTCTGAGAACGGCCTGCTGGCTGTGGAGGCTCTAACAGGGGGTGTGCA
AGCTGCTGCGGCTGGATGACCTTTCATCTGGTGGAGGCATCCCACAGAAGGAGCACTAC
CTGTCAGTGCAACAGCGGCCATTGATACGGGGTATTGTCGCTCTGAGGGTGGAGA
TGGCAAGCTCTTCATCGGCAGGGCTGTGGATGGGAAGCAGGGTACTTCCCGACCCGTCCA
GCCCGAAGCTGGCCCGAGACCTGAGTCTCAGGCCATGCTGACTATAGAGCTACACAGCGAT
TTTGTCTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGCTCTCCACTTTGACAT
CCTCTACATCTACGGCTTGTAGTGGGGCTTTGTCTACTTCTCAGTGTCCAGGGCCAGA
CCCCCTGAGGGTGTGGCCATCAACTCGCTGGAGACACTCTTCAACCTCACGACATGTGCGG
CTCTGCAAGGATGACCCCAAGTTCACTCATCGTGTCCCTGCCCTGGCTCACCGGGC
CGGGGTGGAATACCGCCCTCTGCAGGCTGTTACCTGGCCATCTGGGACTCACTGGCCC
AGGGCTTCAATATCACAGCCAGGAGCATGACTCTGCCCTGTGCTTCCATCTCCAAAGGGCCAGAAG
CAGTATCACCAACCCGCCGATGACTCTGCCCTGTGCTTCCATCTGGGCAACTGGAGCTCACTGGC
GAGATCAAGGAGCGCTGAGTCTGACCCAGGGCGAGGGCAACCTGGAGCTCACTGGC
TGCTGGGGAGGGACGTCAGTGCAGAAGGGCCCTGCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCGTACACCA
CAGCAGGGAGCCATGACCTCTGGCCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAAGGTGGCAAGCTGAAAAGGGTAAGAGTCATGAGTTCAAGTGTCCAAATGCC
ATTCACTCTCAGCAAAGAGTCCCTTGGAGGTAGCTTATGGTGGAGATTAACTATAG
GCAACTTATTTCTGGGGAAACAAGGTGAATGGGGAGGTAAGAAGGGTTAATTGTTG
ACTTAGCTCTAGCTACTCCTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCTAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAA

FIGURE 62

MGTLLGQASLFAPPGNWFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDVSRVVLLSVWVLLAPPAAGMPQFSTFHSENRDWTNFNHLTVHQGTGAVYVGAINRV
YKLGTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLTNVNKLIIIDYSENRLLAGSL
YQGVCKLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPDPPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHYSVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHPPDDSAACFPIRAINLQIKERLQSCYQGEGN
LELNWLKGKDVKCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFGTKSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTCGGACTGGAGATGGGAACCCGGGCCCCCGCCTTAGAGAACACCGCGATGCC
CGTGGAGCCTCGGGCGAGGCCGGGGCACGCTGGGACTCTCTGCTGTGCTCTGGGCTTCCTGGCTCC
GCAGGGCTGAGCTGGAGCACCTGGTCCCTTGCGGCTCCGGCACATGCAAGCTGGGGCTGAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTGAGGATCTTCCGGGGCTCCATCCACTATTTCGGTGTGCCCAGGGACT
GGAGGACCGGGCTGTAAGATGAAGGCTGTGGCTGAAACCCCTACCCACCTATGTTCGGTGAACCTGCATG
AGCCAGAAAAGGGCAAAATTGACTCTCTGGGACCTGGACCTGGAGGGCTTCTCTGTGATGGCCGAGAGATCG
GGCTGTGGGTGATTCTGCCTCCAGGGCCCTACATCTGCACTGGAGATGGACTCTCGGGGCTTCGGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGGAGCTGAGGACAACCTAACAGGCGACCCAGGCAAGCAGTGGACCTTTAATTGACCA
TGATGTCCAGGGTGGTGGCACTCCAGTACAAGGCTGGGGACCTATCATGGCGTGCAGGTGGAGATGAATATG
GTTCTATAAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGACTCTGGAGGACCTGGCATGTGGAACTG
TCCTGACTCAGAACACAAAGGATGGCTGAGGAAGGGGATGTCAGGGGACTTGTGGCCACCCATCAACTG
CAACACA CGAGCTGCGACTCTGACCAACCTTCTCTCAAGCTCCAGGGACTCAGCCCAAAGATGTGATGGAGT
ACTGGACGGGGTGGTTGACTCTGGAGGG
CTGGGCACTTGTGGACCGGGCTCTCCATCAACCTCTACATGTCCTCCAGGGGACCCAACTTGGCTCATGAATG
GAGCCATGCACTTCCATGACTACAAGTCAGATGTCACCGACTATGACTATGATGCTGTGCTGACAGAACCGGGG
ATTACAGCAGGAAAGTACAGTGGCTGAGGACTCTGGCTCTCCCTCAGGCAATCCTCTCCCTCCCCAACCTG
ACCTCTTCCAAGGAGTGGCTGATGACCCCTTAACGGCAGCTTGTACTCTGCTCTGAGGACGCCCTCAAGTACC
TGGGGGAGGCAATCAAGTGGAAACCCGATCAACATGGAGAACCTTGTGAACTGGGGAAATGGACAGTCT
TCGGGTGATCATCTCATGAGAACCGGACATCACCCTGTGGCACTCTGAGTGGGACCTGGCTGAGGGGGGGGG
TGTGTTGAAACAGATACATAGGATTCTGGACTACAAGAACAGAACAGATTGCTGTCCTCCCTGATCCAGGGTT
ACACCGCTGCTGGAGATCTGGTGGAGAATCTGGGGGAGCTAACATTGGGGAGAATATTGATGACAGGCAAG
GCTTAATTGGAAATCTCTTATCTGAATGATTGACCTCCCTGAAAATCTGCAATGCTGGATATGAAAGA
GCTCTTCTTCAAGGGCTGGCTGGCAAAATGGNNTCTCCCTGGAGAACATACCTGGTCTTCTCTCT
GTAGCTTGTGCTCATGAGCTCCACGGCTTGAGACCTTCTGAGGACTCTGGAGGCTGGGAGAAGGGGGTGTGATTCA
TCAATGGGAGAACCTTGGACCTTACTGAAACATTGGACCCAGAACGAGCTTACCTCCAGGTCCCTGGTGTGA
GCAGGGAAATCAACAGGTCATCTGTTTGAGGGAGGAGCTGGGGGCTCTGCAATTACAGTTCAGGAAACCCCCC
ACCTGGCAGGAAACAGTACATTAAGTGAAGCTGGGCTGGGACCCCCCTCTGGCTGGTGCAGTGGGAGACTCCGGCTC
CTCTGGACTCTGGGCTGGCTGGCTGGGCCCCCTCCTACGCAAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG
TGGCTTCTTGTGATGATGGCTTCTACAGGGCTGGCTTGAGGAGGCTGGGCTGGCTGGCTGGCTGGCTGG
AGCTAATCAGATGGCCAGGCTTGGGCTTCTGAGAAAATGCTGAAACCTGGGGGCTTGTGACGGTCAAGCCC
TGGAGCATCTGCTGGACTCTGGGCTGGCTCTGGCTGGTCTTCTGGGGGGCTGGGACATCCCTCATGGCC
TTATCCGGGAATCTGGGTTGTCACCAAGTGTAGGGGTTGGGAAGGGGTGTCACCTGAGCTGACCTTGT
CTTCTCTACACCTCTGAGCTTCTGGGATTCTGGAGAACACTGGGCTGAGAACATGTCACCTCC
TCCCTTCCACTCTGGCTGCTTCCCAAGGGTGACAGGGCTGGGCTGGAGAACAGAACATCTCCTGGCTCTTCC
CAAGTGTAGGGGTTCTGGTGTGAGTGGAGGAGACATGTGAGTCTGGCAGAACCCATGGCCATGTCACATCC
CATCCAGGGAGGAGGAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACCCATGGCCATGTCACATCC
AGGGAGGAGGAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACCCATGGCCATGTCACATCC
GGAGGAGGAGAACAGGCCAGCTCACATGTGAGTCTGGCAGAACCCATGGCCATGTCACATCC
ACAGAAGGGCCAGCTCAGTGGCCCCGGCTCCACCCACCCACGCCAACAGCAGGGGAGAGCAGGCC
GAAGTGTGTCAGTCCAGTCCGATTGAGCTTGTGGGGCCAGGCCAACACCTGGCTTGGCTACTG
GTTGCACTGAAAGCTATAACCTGAATCACAA

FIGURE 64

MTTWSLRRR PART LGLLL VVLGFLV LRRLDWSTLVPLRLRH RQLGLQAKGWNFM LEDSTFW
I FGGSIHYFRVPREYWRDRLKMKACGLNTLTTYV PWNLHEPERGKF DSGNLDLEAFVLM A
AEIGLWVILRP GPYICSEMDLGGLPSWLQDPGMRLRTTYKGFT EA VDLYFDHLM SRRVPLQ
YKRGGPIIAVQVENEYGSYNKDPA YMPVVKKALEDRG IVELLLTS DNKG LSKGIVQGV LAT
INLQSTHELQ LTTFLF NVQGT QPKMVMEYWTGWFDSWGGPHNILDSS EVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVT SYDYDAVLTEAGDYTA KYMKL RDFFG SIS GIP
LPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVN GNGQSF GYI LY
TSITSSGILSGHV HDRGQVF VNTVSIGFLDYKTTKIAVPLI QGYTVL RILVENRGRV NYGEN
IDDQRKGLIGNLYLNDSPLKNFRIYSLD M KK SFF QRFGLDKWXSLP EPTPLPAFFLG SLSIS
STPCDTFLKLEGWEKGVV FINGQNLGRYWNIGPQKTLYLPGPWLS SGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

FIGURE 66

MAPKKLSCRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLHYHNGGNIIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQGNHSTRSVSAVTKGLENMLKLGA SVNM MYMFHGGTNF
GYWNGADKKGRFLPITT SYDYDAPISEAGDPTPKLFALAR DVISKFQE VP L GPL PPPS PKMML
GPVTLHLVGHLLAFLD LLLC PRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHD RAYVMVDGVFQGVVERNMRDKLFLT GKL GS KLD ILEN MGRLSFGSNS SDFK GLLKP
PILGQTILTQWMMFPLKIDNLVKNWFPQLPKWPY PQAPSGPTFYSKTF PILGSVGD TFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGTG
ACCCACAATATGGCTTACATGTTGAAAAAGCTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACTTGAAGGAATATT
CTTCGAAAAGTCAGAGAAGAGAGCAGTTTAGTGACATTCCAGATGTCAAAACGATTT
GCGTTCCCTCTCACATGGTAGACCAGTATGACCAGCTATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAAACATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAGCAGGAGTTGCATCTGTCATG
CTGTCGGGGTGCCTGATGCTGCTTGCACCTCACAGACCTGGATGCTAAAGCTTGAAC
AATTCCAAGCTAAAATTCTGTAAGATTCTCAATGACTAACCTCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTTCACGTGAAGTCACTGATGTTGGCTGAAATTCTGCTGGGTGATTGCTCAAAA
CCTCGAGAGTTGACTTAATAGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGACCTTAAGATTCTCCACGTGAAGAGCAATTGACCAAGTT
CCCTCCAACATTACAGATGTTGCTCACATCTACAAAGTTAGTCATTCATAATGACGGCAC
TAAACTCTGGTACTGAAAGCCTTAAGAAAATGATGTAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTTTAGCTGCTGAGCTGAACTGGAT
TTAAAGTCCAATAACATTGCAACATTGAGGAATCATGAGTCCAGCATTAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACCTTATTCTCAACACAAAGCTGCAATCCTTACAGTGGCAGTATT
AGTTTACAGAAACTCAGATGTTAGATGTGAGCTACAACAACTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCACTGCTGATATCACTGGGAAACAAAGTGGACATTCTGC
CAAACAAATTGTTAAATGCAAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC
TCACCTCCAGAGAAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCTGCCAGCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTGTTG
TGAAGATCACCTTTGATACCCGCCACTGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAATGGGATTAAACTAAGATAATATGACAGTGATGTCAGGAAC
AACTTCCTAGATTGCAAGTGCACGTACAAGTTATTCAAGATAATGCATTAGGAGTAG
ATACATTTTAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGTTTAAGTCATTCAATTCAAATCATTGTTCTTTGGGG
AAAGGGAAGGAAAATTATAACTAATCTGGTTCTTTAAATTGTTGTAATTGGAT
GCTGCGCTACTGAATGTTACAATTGCTGCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKLNRELHYLIGNLNSENNKMIGLESLRELRLKLILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS
NNIRTIEEEIISFQHLKRLLTCLKLWHNKIVTIIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRLCDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRLPAQLGQCRMLKKSGLVEDHLFDTLPLEVKEALNQDINIP
PANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCGGGCTTCTCTGGACTTTGCATTCATTCTTCATGGACAACTGACTTTTATTC
TTTTTCCATCTCTGGCCAGCTTGGATCCTAGGGCCCTGGGAAGACATTGTGTTTACACATAAAGGAT
CTGCTGGTGGGTTCTCTCTCCCTGGACATTGGCATTTGCTTACTGGTGTGGGAGGGAGACCACTGG
GCTCAGTGTCTGCTGCACTTATCTGCCAGGTACATCAAGGTCTTGTGACCTAACACTGATTATGCC
ATCGCTGGTGTATCTGGCGGCCCTGCTGCCCTGCTGATAGTTGCTGTCTGCTTACTTCAAAAACACAAC
GCGCTTAAAGCTGCAAAAGGAACTCTGAAGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
AGTTTGATTCCCTGCCACCTCTGCTTGGACATAATGGGGCCCTGAGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGCCCTGAAGACTTCATGATGCAATGAGGGGCAACTGTGTGATGTGAGGCAAGAAGGACAG
CTCCCCATCAGTTATGGAAAATAACTCAGTGCTGCTGGGAAACCGAGCTGCTGAGATCCTACAGAGAGCTTC
CACCTGGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGAATGTGATAACCCAGTCA
CACAGCTCTTATTCACAAAATCTACCCCTTGGCTGGCTGACGTGACGTTCTGGAGGTGCTCAGAAA
GCTGATGTAACACAGGCTTAAAGCTGCTGGCTTAAAGCTGCTGGCTTAAAGGCTGGCCTTCCAAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCTCTTAAATCTCTCTGTTGGGGAGCTGACAAATGGGAGCTGAGGCAAT
GCAAGCTGCGACAGCTAGCTAGGGGTGCCAATATGGCAGAGGCCAACAAAGCCATGATCTGCAACTCAATCCC
AGTAGAGACTGCACCTGGACATAAGAAAGCAGGAAACAAAGCATGAGAATTATCTTCTTCTATGTCAGCTT
GATCCAGATGGAAAGCTGTAAGAACTTAAAGACTTGTGTTGAATCATCTCCAGTCAATTGACGTTTCAAATAGTTACT
CAAGTCTGCACTTAAAGGACTGTTCTGTTGAATCATCTCCAGTCAATTGACGTTTCAAATAGTTACT
GACTCAGGAAGAATTCAAAAGACTGTTCTGTTGAATCATCTCCAGTCAATTGACGTTTCAAATAGTTACT
GGCGGTACCTGGATACCTGGAAAGGATCTTCACAGCCCCAATTACCCAAAAGCCGATCCTGAGCTGGCTTAT
TGTGTTGGACATACAGGAAAGGATACAGGAAATACAGGAAATACAGGAAATACAGGAAATACAGGAAATACAGGAAAT
AAACAGTGCATAATTGATTTCTGCCACATCTGATGCCCCCTCCACCAACTCTGGCTGATTTGACAAAGTCTG
GGCGGTGACTGCCACCTGATCAACTTACAGTCTGCTGTTGCTACAGGTTATGCGCAATTCT
TACCGGGGATTTCCTGCTCTACACCTCAATTATGACAAACACTACATCTTAACTTGTCTCTTCT
GACAGGTGAGAGTATTATAAGCAATCTACCTAGGGCTTTAACTTAACTGGGAAATACCTGGCAACTAAAA
GACCCAACTTGGAGCAAAATATCAAATGTTGCTGAAATTCTGTCCTCTTAAATGGATGTGACATCAGA
AAGGTAGAGATCAGTCATTAACCAATAATCACCTTCTGATCTCAACTCTGAACTGATCACC
CGTAGAGAAACACTCCAGATTATGTAAGCTGTGAATGGGACATAATTCTACAGTGAGGAGATAATATACATAAACA
GAAGATGATGTAATCAAAGTCAACTGGCAATAAACACCAAGCATGGCTTCTTGTGATCAAATICA
TTGAAAAGACTTACCTGAATCACCATAATTGTTGAGGTTTGTGAACTTCTTGTGATTTGCAAGTTAGTCTGCAC
ACCTCAGATCCAATTGTTGGTTCTGTGATACCTGTAAGGCTCTCCACCTCTGACTTTGATCTCTCAAC
TACGACCTAATCAAGAGTGGATGTAGTCAAGATGAACTTGTGTAAGGTGATCTCTTATTTGGACACTATGGGAGA
TTCAGTTAAATGCCCTTAAATTCTGAGAAGTATGAGCTGTGATCTGAGCTGTAAGTTTGTGATCTGAT
ACGAGTACACCAACAGCTCTGCCATCAAGGTGTTCTCAGAACGAGAACACTTCTTCTATATAAATGG
AAAACAGGATCCCATAGAGGCCATTCTGCTGAAAAGGGATCGAGTGGCAAGTGCAATTCAAGGATTTCAGCAT
GAACACATGGGAAAGAAACTTCAAAACAGCCATTCAACAGTGTGCACTGTTTCTCTGATGGTCTAGCTG
AATGTGGTACTGTAGCGACATCACAGTGAGGCTTTGTAAATCAACGGGAGACTACAAATACCAAGAAGCTG
CAGAACTTAACTAACAGGCTCAACCCCTAAGTGAGACAATGTTCTCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATATGAAATGAAGGAAAGGCTGAAAGTGCACACAGGCCCTGCACTAAAAAA

FIGURE 70

MELVRRLLMPLTLLIILSCLAEELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPEENCTWTI
ERPENKSIRIIIFSYVQLDPDGSCESENIKVFDGTSSNGPILLGQVCNSNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTFPTFESSSSNLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSEDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSPVPLNGCGTIRKVEDQSITYTNITTSASSTEVITRKQQLQIIVKCEMGHNST
VEIYIITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPTYVVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL
QCKVLI CDSSDHQSRCNQGCVSRSKRDISSYKWKTDSIIGPIRLKRDRSAGNSGFQHETHA
EETPNQPFFNSVHLFSFMVLALNVVTATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGCCCTGCGCCG
GGAC**ATG**CGGCCCCCAGGAGCTCCCAGGCTCGCTTCCCGTGCTGTGCTGCTGC
TGCCTGCCGCCGCCGCGCTGCCACAGGCCACGCCCTCGCACCCACCTGGGAGTC
CTGGACGCCGCCAGCTGCCCGCTGGTTGACCAGGCCAGTCGCATCTTCATCCACTG
GGGAGTGTTCCTCGTCCAGCTCGGTAGCGAGTGTCTGGTGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAATTTTTAATGCCAACAGTGGGAGATATTTCAGGC
CTCTGGTGCCAAATACATTGCTTAACCTCCAACATCATGAAAGGCTTACCTTGTGGGGT
CAGAATATTCTGGTAACCTGGCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCATTAGGAACAGAACCTGCCTCGTGGACTGTACTATTCCCTTTGGA
ATGGTTTCATCGCTTCCCTGAGGATGAATCCAGTTCATTCCATAAGCGGAATTCCAG
TTCTCAAGACATTGCCAGAGCTCTAGTGGTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAACTGGAACAGCACAGGCTTCTGGCTGGTT
ATAATAAGAACCCAGTCGGGCACAGTGTACCAATGATGTTGGGGAGCTGGTAGCA
TCGTGAAGCATGGTGGCTTCTATACTCTGCACTGTATCGTTATAACCCAGGACATTTTGCA
CATATAATGGGAAAATCTGACATAAGACAACACTGTCCTGGGGTATAGGAGGGAACTGG
AATCTCTGACTATCTTAACTTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTGTG
GAGGAATCTTTGATGAATATTGGGCCACACTAGATGGCACCATTCTGTAGTTTGTG
GAGCGACTGAGGCCAAGATGGGCTCTGGCTAAAGCTAATGGAGAAGCTATTATGAAACCTA
ACCTGGCGATCCCCAAGATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGCCACATCAGGACAGCTGTTCTGGCCAT
CCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTCTTGGAGCAAATGGCATTATGGTGAAGCACTGCCACAGCTAACATTCTCATGATGC
CGTGTAAATGGGCTGGCTACGCCCTAACTATGGTGAAGCT**TAAAGT**GCAGCAGACTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGAACTGGATAAGAAAATTATTGGCAGTTAGCCCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTTAACTCTCAGTGCATTGGCATTAAAGTC
TCTTCACATTGATTCTTCATGTGTACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGGTGAAGCCATATCCCCCATG
ATTATATAGTTATGCACTTAATATGGGGATATTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTGTGGCAACATCATAGAGTGTATTACAAATCTAGATGCCATAGCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACTGATGTACTG
AATACTGTAGGCAATAGTAAACAGTGTATTGTATATGAAACATATGGAAACATAGAGGAAG
GTACAGTAAAATACTGTAAAATATGGCAGCTGTATAGGGCACTTACCAAGATGGGAG
CTTACAGGACTGGAAAGTGTCTGGGTAGTCAGTGAGTGAATGTGAAGGCTAGGACATTA
TTGAACACTGCCAGACGTTAAATACTGTATGCTTAGGCTACACTACATTATAAAGAAAAAA
GTTTTCTTCTTCAAATTAAACATAAGTGTACTGTAAACTTTACAAAACGTTTAAATT
TTTAAACCTTTGGCTTTGTAAATAACACTTAGCTTAAACATAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFLPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSPFGSEWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFVNANQWADIFQAS
GAKYIVLTSKHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHWKWCNCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSLKVNGEAIYETYT
WRSQNNDTVTPDVWYTSKPKEKLVYAIFLKWPMSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWLALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

T00720 * 255820660

FIGURE 73

AGCAGGGAAATCCGGATGTCGGTTATGAAGTGGAGCAGTGAGTGAGGCCCAACATAGT
TCCAGAACCTCCATCCGGACTAGTTATTGAGCATCTGCCTCATATCACCGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAGGGGTAGGCACGATGCCAGGTGCTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACAGGGCTCTGGTCCAAGGCTTTGCGTGCAGAAAGAGCT
TTCCATCCAGGTGCTAGCAGAAATTATGGGATCACCCCTGTGAGCAAAAGGGCGAACAGC
AGCTGAATTTCACAGAAGCTAGGAGGCTGTAGGCTGTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTTGGAGA
TGGATTCTGTGATCTCTAGGATTAGCCCAAACCCCAAGGTGTTGAGGAAAAATGGGGTGGGTG
TCTGTAGTTGAAGGTTCTGGTGCAGCTTGAGCCTATTGTTACAACCTCATCTGAT
ACTTGGACTAACTCTGTGATTCAGAAGAAATTATCACCAAAAGATCCCATATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTGAGCTGACACTACCTACTCGGTGCCATCCCCCT
ACTCTAACATACTCCCTTAACACTACTCTCTCTGCTCAGCTTCCACTCTTACACCG
AGAAAAAAATTGATTGTGACAGAAGTTTATGGAAACTAGCACCATGTCTACAGAAAC
TGAACCATTTGTTGAAATAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTC
CCACGGCTCTGTGACTGTGCTCTCTCTGGTCTGCTGAGCTGCTGGTCTGGATTTC
TATGTCAAAGGTTATGTGAGGCTTCTCTTACAAACAGAATCAGCAGAAGGAATTGAT
CGAAAACCAAGTACTAAAGGAGGAGAAGGCAATGATGCAACCCTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGGAAACTACCGTGCAGTGCCTGGAA
GCTGAAGTTAGATGAGACAGAATGAGGAGACACACTGGAGCTGGTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGAAATCAGAAGGCAAAAGAACCAAAGAAGAAAGTCCACCCCT
GGTCTCTAACTGGAAATCAGCTCAGGACTGGCATTGGACTATGGAGTGACCAAAGAGAATGC
CCCTCTCTTATTGTAACCCCTGCTGGATCCTATCCTCACCTCAAAGCTCCACGGCC
TTTCTAGCTGGCTATGCTCTTAAATATCCACTGGGAAAGGAGTTTGCAAAGTGCAA
GGACCTAAACATCTCATGCTACTGGCTAAAGGCTCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGGCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCGCAGCTCAGAC
CCCTTCTCAGCTCTGAAAGGAGAACACGTATCCCACCTGACATGCTTCTGAGCCGGTA
AGAGCAAAGAATGGCAGAAAAGTTTAGCCCCGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTGTAAAGCTAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAACACACAGACAGGGTAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACTTACTTTCTGGTCTACACTGCTGATATTCT
AGGAAATAACTTACAGTAAACAAAATAAAAACCTTAAATTCTATTCT
GTTACAGAAATGTTACTAAGGAAGGATTACTGAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAAATATTCTCTAAAGGCAACATAGTAGAACGCTATCTGGGAAGCTATTCTTCA
GTTTGATATTCTAGCTTACTTCAAAACTAATTCTATTCTGAGACTAATCT
ATTCATTTCTCTAATATGGCAACCTTAAACCTTAATTATTAAACATACCTAAGAAG
TACATTGTTACCTATACCAAAAGCACATTAAAAGTGCCTAACAAATGTATCACTA
GCCCTCTTTCCAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAAATTAA
AGCATTAGAAAACCTT

FIGURE 74

MARCFSLVLLTSIWTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTAKEAECR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNNPKCGKNGVGVLIWKPVPSRQF
AAKYCNSSDTWNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVSPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCAATTGCTCTCGTATTGGTGCACGACTTCACGATGG
CTCGCCCAACCTTAACCTTCTGTCGGCCCTGCTCTGCTGCCCTACTCGTAGGGAA
ACTGCGCCGCTCTGCCACGGCTGCCCCACCGAAGACGGTAACCGTGTGACTTTG
ACTGGAGAGAAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAAGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCACTGGCCACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACCTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTGC
TTGGTCTAATGACTGCAATCATTGCCCTATCATGTCACCTCCCTAAATACAAC
GTACAGGGCTAAATTGGAAAGGTGGATTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGACCAACATCACCCCTACCAAGCAACTCCCTACCCGTACCTGTTCCAAGGG
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACACAGTCAGA
TGGGAAAACAAGAAGGATAAATAAGATCCTCACTTGGCAGTGCCTCTCCTGTCATT
CCAGGCTCTTCCATAACCAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTCTGATTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCAACTGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGAAATGGTTCCCTCAAGCTGGTCAGTGTGTTAAGTGCCTTAC
AGCTATTCAAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCCCTT
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGT
CGCTAAGAATTCCCCAAGGACTCTGCTTCAAGCCCTCTGGCTCGTTATGGTC
TTCACTAAAGTATAAGCCTAACCTGCTGCTAGTCCTAAAGGAGAAACCTTAACCAAAG
TTTTATCATTGAAGACAATTGAACACCCCCCTATTTGTGGGGATTGAGAAGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGTGGTAGGACTTGGAGGAGAAACCCCTGGACTTCAC
TAACCCCTCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAAATAAGATTGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSPRRLSRWLAQPYYLALLSAFLVRLPPLCHGLPTQREDGNPCFDW
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEEELERDKRVTVIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTQQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG
GGCCCCCAGCTGGCCGGGTCAACCTGGCATAGGGAGAGGGCTGTTGCTCCTGGTCCA
TTGTCCTGCTGCCGGCTCTACGGACTGCCCTCTACAACGGCTTCACTACTCAAACAG
CGCCAACGACAGAACCTAGGCAACGGTCAATGGCAAAGACCTCTTAATGGAGTGAAAGCTGG
TGGTGGAGACACCCGAGGAGACCCGTTCACCTACCAAGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCGCGGCGTGTGCGTCAAATGGTGAAGCT
GTGCGAGAACGGGGCCCAGAGAAGGACGTGCTGGTGGCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCGCGTGCACCTGCCGGAGAACAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCCGGGTGTTCTTCTTACAGTCCCCCA
ACGGGGCCTACAGTCACCTCCACGGGGCCAGCAGGCTGTGCCAGGAGCAGGCTGCCGTG
GTGGCCTCTTGAGCAGCTTCCGGCCTGGAGGAGGGCTGGACTGGTGAACCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGGCC
CAGGCCCTGCCACCTGGCGTGCAGAGCTACGGCCCCGCCACCGCCCTGCACCGCTATGAT
GTATTCTGCTCGTACTGCCCTCAAGGGCGGTGTAACACTGGAGCACCTGAGAACGCT
GACGCTGACAGAGGCAAGGGAGGCTGCCAGGAAGATGATGCCACGATGCCAAGGGGG
AGCTCTTGCCGCTGGAAGTTCCATGGCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTTGACCCGATCTTAACGTGGGCCCCAGAGCTGGGGT
CCGAAGCTTGCTTCCCCGACCCGAGAGCCGCTTGTACGGTTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCTGCCGATCCCTCACTGGCTGTATTGAGTGGTT
CGTTTCCCTGTGGGTTGGAGCATTAACTGTTTATACTTCTCAATTAAATTTCT
TTAACACATTTTACTATTTTGTAAAGCAAACAGAACCCATGCCCTTGTGCCCTG
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGGCCATTGCGGTTTGTGGCTCTG
GAGGGTTCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGGG
GGTGGCCTGCTAGAATGCCGGAGTCCGGCATGGGGCACAGTTCTCCCTGCCCT
CACCTCTACTTCTGTGAAGGCCGTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCAGGCAGAACATCTGAGGGAGGAAGAAAACCTCCCTCCCGTT
TCCCTCTCGGTTCAAAGAACATGTTTGTGTCATTGTTCTCTGTTCCCTGTTG
GGAGGGGCCCTCAGGTGTGTACTTGACAATAATGGTCTATGACTGCCCTGGCAA
AAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 78

MGLLLLVPLLLPGSYGLPFYNGFYYNSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRLRHSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFYQSPNGRYQFNFHEGQQ
VCAEQAAAVVASFEQLFRAWE EGLDWNCAGWLQDATVQYPIMLPRQFCGGPGLAPGVRSYGPR
HRLLHRYDVFCATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKGQLFAAWKFHGLDR
CDAGWLADGSVRYPPVPHPNCGPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

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FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**GATGATGTGGCGACCAC**TCAAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCAGACCGAGGCCCATGGC
CAGGGGAGGGTGCACCAGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCAACGGAA
CTTCAGTAGACCATGAGGCTTCTGGAGGGAAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAGCCAGGCCGCTGGGGCGATCGTGACCGCATGGACGCCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCGAGCTCGCGCTGGATCGGCACACGAGCAGCGGC
CATACGGGACTCGGTGAGCGCCCTGGGACACGTACGACACGGACCCGACGGCGTGTGG
GTTGGAGGGAGCTGCGCAACGCCACCTATGGCACTACCGGCCGGTGAAGAATTCTGAC
GTGGAGGATGAGACCTACAAAAGATGCTGGCTGGGACGAGCGCGTTTCCGGTGGC
CGACCCAGGATGGGACTCGATGGCCACTCGAGAGGAGCTGACGCCCTTGACACCCGAGG
AGTTCCCTCACATGGGACATCGTATTGCTGAAACCTCTGGAGGACCTGGACAGAAA
GATGGCTATGTCAGGTGGAGGAGTACATCGGGATCTGACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCTGGGTGAGACGGAGGGCAGCAGTTCCGGACTTCCGGATCTGAAACAAGG
ATGGGCACCTGGATGGGAGTGGGTGGCCACTGGGTGCTGCCCTGCCAGGACAGCC
CTGGTGGAAAGCCAACCACCTGCTGCACAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
ACGGAAATCTGGTAATTGGAACATGTTTGTCAGCTGAGCCACCAACTATGGGAGG
ACCTGACCCGGCACACGATGAGCTG**GAGCACCAGC**ACCTGCCACGCCCTAGAGGCCG
ACAATGACGGAGGAGGGCCGCTGTGGTCTGCCCTCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCCAAGGCATCCCTGCCCTGGGCTCTCAGGGACCCCTGGGTGGCTTC
TGTCCTCTGTCACACCCCCAACCCAGGGAGGGCTGTCTAGTCCCAAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGGCCAGACCCAGGGACCCCTGGGCTCAAGCTCAGCTCTAA
GAACCGCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACACATAGACTGAAACTCCCT
GGCCCCAGCCCTCTGGCTGGCTGGACACCTCTCTCTGCCAGGAGGAATAAA
AAGCCAGCGCCGGACCTGAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MWWRPSVLLLLLRLHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPPEESQARLGRIVDRMDRAGDGWVSLABELRAWIAHTQQRHIRDGSVAADT
YDTDRDGRVGWEELRNATYGHYAPGEFHVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDILNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESDTDKDGRSLKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

T0017015820660

FIGURE 81

GGGGCTTGCCTTCGCACTGGGCGAGGGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGGGTGCAGGGATCCCTGACGCCCTGTCCTGTTCTTGTCGCTCCAG
CCTGTCGTCGCTGTTTGCGCCCGCCTCCCGCGTGCAGGGGGTGCACACCGATCCCTG
GGCTTCGCTCGATTGCGCCGAGGGCCTCCAGACCTAGAGGGGCCCTGGCTGAGCAG
CGGGTCTGTCGCTGTCCTCTCCGGCGCCGGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACCGCGGGCCTCCCGCACCTGGCTGCCCCATTCTCCCTCTCCAG
GTGTGAGCACCTATCAGTCAACC**ATG**TCCGAGCCTGGATCCGGCTCGGCCCTGGTGTG
TGTCTGCTGCTGCTGCCGGGCCGGCAGCGAGGGAGCCGCTCCATTGCTATCACATG
TTTACAGAGGCTGGACATCAGGAAGAACAGAGTGTCTCTGCCAGGGGCTGCC
CTCTGAGGAATTCTCTGTATGGAAACATAGTATATGTTCTGTATCGAGCATATGTGGG
GCTGCTGCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATGCCACC
TGGTCGAGAAACTATCTCTCAGTAGATGCCAATCCAGTCTCAATGCTTCTAGAT
GGTCTGCTTCTTACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAGCA
GTGTCACAGCACATCACCACAGTAAACGACTAAAGAAAACACCCAGAGAAGAAAATGG
CAATAAAGATGTAAAGCAGACATTGCAATTGATTGATGGAAGCTTTAATATTGGCAGC
GCCGATTAATACAGGAAGTGGCTTAAGGCTTAATGTTGGAAATTGGAAACA
GAAGGACCCACATGTGGGCTTGTCAAGCCAGTCAACATCCAAAATAGAATTTCAGTGA
AAACTTTACATCAGCCAAAGATGTTTGTGCAAAAGGAAGTAGGTTCAGAGGGGTA
ATTCACAAACAGGAAACCTTGCACACTGCTCAGAAATTCTTACGGTAGATCTGGA
GTAAGAAAAGGGATCCCAAAGTGGTGGTTTATTATGGTGGCTTCTGATGACAT
CGAGGAACAGGGCATTGCCCCAGAGAGTTGGTGTCAATGTTATAGTTCTGGCCA
AGCTTACATCCCTGAAGAACGGGATGGTCAGGATGTCAATTGTTGACAAGGCTCTGT
CGGAATAATGGCTTCTCTTACACATGCCAACTGGTTGGCACCACAAAATACGTA
GCCCTGTTGACAGCTGCACTCATGAACAAATGATGTCAGCAAGACACTGTTAACT
CAGTGAACATTGCTTCTAATTGATGGCTCCAGCAGTGGAGATAGCAATTGCCCTC
ATGCTGTAATTGTTCCACATGCCAACACTGGAAATCTGGACATTGGTGGCAAGAT
AGCTGCTGACAGTTTACTTATGATCAGGCCAGGAGTTCAAGTTCACTGACTATGCC
AAGAGAATGCTCTAGCTGTCACTAGAAACATCGCTATATGAGTGGTGAACAGCTACTGGT
GATGCCATTCTCTTCACTGTTAGAAATGTTGGCTTGGCCATAAGGGAGAGCCCCAACAGAA
CTTCTAGTAATTGTCACAGATGGCAGTCTTATGATGTCAGGCTTCAAGGCTTGCAGCTG
CACATGATGCCAGGAATCACTATTCTCTGTTGGTGTGGCTTGGGACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACCGTTCTTACAAGAGAGTTCAACAGGATT
AGAACCAATTTGTTCTGATGTCATCAGAGGCAAGGGCATTGAGATTTCTAGAATCCAGCAAT
ATGGTAAACATTGACAACAGGAAAGTACAAGGGATCCAGTGTGTAATTGATT
CTCATAAACTGAAATGCTTCTGATGCAACTAGAATCAGATAACAAACTATTAAGTATGTCAC
AGCCATTAGCCAAATAAGCACTCCCTAAAGGCCCTGCCCTCTGGTTACAATTGCAAGTGT
ACTTTGTTAAAAACACTGCTGAGGCTTCAATATGCTTCTAGAAGACTCAGGAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTCTAACCATGCTACTAAATGATCAGATAATGCCAA
TTCCATAGCTCAATAAGAATCTGATACCTAGACCAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGKDCDKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPVHGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNFIIVSVAKPIPEELG
MVQDVTFVDAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIACLI
DGSSSGVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLA
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVITDGQSYYDVOGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CCCGCGCCTCCCGACCCGGGCCCCCGGCCACCGCGCCGCTCCGCATCTGCACCCGAGCCC
GGCGGCCCTCCGGGGAGCGAGCATCGAGATCCAGTCCGGCCCGAGCGCACTCGTCAGTC
GGCGGCCGCTCGGGCGAGAGCGAGATGCAGCGGCTTGGGCCACCTGCTGTGCCCTGC
TGCTGGCGCGGGTCCCCACGGCCCCCGGCCGCTCGACGGGACCTCGCTCAGTC
AAGCCGGCCCGCTCAGCTACCCGGAGGAGGCCACCCCTCAATGAGATGTTCCGGGA
GGTGAGGAACTGTGGAGGAACAGCAGCACAAATTGCGCAGCGTGGAAACTGGCAA
CAGAAGAACGCTGCTGCTAACGATCATCAGAAGTGAACCTGGCAA
ACAATGAGACAAACACAGACAGAAGGTTGGAAATAACCATCCATGTGCACCGGAA
TACAAGATAACCAACCAACGACTGGAAATGGTCTTTCAGAGACAGTTACATCTG
TGGAGAGCAAGAACGGCAGAGGAGCCACGGTGCATCATCGACGAGACTGTGGCCCG
ATGTACTGCAGTTGCCAGTACACCTGCCAGCCATGCCGGGCCAGGGATGCT
CTGCACCCGGACAGTGCAGTGTGGAGGACAGCTGTGTCTGGGGTCACTGCACAAA
TGGCCACCAGGGCGAGCAATGGGACCATCTGTGACAACCAGGGACTGCCAGCGGCTG
TGCTGTGCTTCCAGAGGGCTGTGTTCCGTGTGACACCCCTGCCGTGGAGGGGA
GCTTGTGCGATGACCCGCCAGCCGGCTTGTGACCTACACCTGGAGCTAGACCTGTG
GAGCCTTGAGCGATGCCCTGTGCGACTGGCCTCTGTGACAGCCCCACAGCCACAGCCTG
GTGATGTGCAAGCGACCTCTGTGGGAGCCGTGACCAAGATGGGGAGATCTGTGCG
CAGAGAGGTCCCAGATGAGTATGAAGATTGGCAGCTTCAGGAGGAGGTGCCAGGAGCTGG
AGGACCTGGAGGGAGGCTGACTGAAGAGATGGCCTGGGGAGGCTGCCGGCTGCCCGCT
GCACTGTGGGAGGGAGAGATTAGATCTGGACCAGGCTGTGGTAGATGTGCAATGAA
ATAGCTAATTATTTCCCAGGTTGTGCTTAAGGCTGTGGCTGACCAGGCTTCTCTACA
TCTTCTCCAGTAAGTTCCCTCTGGCTTGACAGCATGGGTGTTGCATTTGTCAGC
TCCCCCAGGCTTCTCCAGGCTTCAGGCTTCAAGCTGGTGTGGAGACTCAGGAGCCGTAAAC
TGCAGGAGCAGTTGGCCACCCCTGTGCGATATTGGCTGCTTGCCTTACAGTGGCAG
ACAGCGTTGTTCAATGGCTTGTGATAATTGTTGGGGAGGAGATGGAAACATGTGG
AGTCTCTCTGTGATTGGTTGGGGAAATGTGGAGAGATGGCCTTGCAAACATCAA
CTTGGCAAAATGCAAAATGAATTTCACCCAGGTTCTTCCATGGCATAGGTAGCT
TGCCTTCAGTGTGCAGGATGAATGTTCTGTCACCCTCGATTACATGTGTTTATTCA
ACAGTGTGTCAGCTCTACCTCTGTGCCAGGGCAGCATTTCATCCAAGATCAATT
CTCTCTCAGCACAGCCTGGGGAGGGGGTCATTGTCCTCTGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCTGCGCAAGCTGCTGCCAAGTCAACACAGCTAGTGAAAGACAGAGCAGTTCT
CTGGTTGTACTCTAAGCTCAGTGTCTCCACTACCCACACAGCAGCTTGGTCCACCA
AAGTGTCCCCAAAAGGAAGGGAGAATGGGATTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAATAATTCTCACATCCCTTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTC
AGTGTGGGGCAGCGTCTTCTAATGAAGACAAATGATATTGACACTGCCCTTGGCAGT
TGCATTAGTAACTTTGAAGGTATGACTGAGCTGAGGCTAGACAGGTTAACCTGCAAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTAAAATGAAATTGCAAAATCATTAGCAGCAAC
TGAGACAATTATCAACAGCTGGGAAATCAAACCGAGCAGGGCTGTGAAATGTT
GTAATATGCGACTGCGAACACTGAACTGAACTCACGCCACTCCACAAATGATGTTTCAGTTGTCA
TGGACTGTGCACCACCATGTATTCATCAGGAGTTAAGTTAACAGTGCACATGATTGTA
TAAGCATGCTTCTTGATTTAAATTATGTATAAAACATAAGTTGCATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLPLPSYHNETNTDKVGNNTIHVRREIHKITTNNQTG
QMVFSETVITSGDEEGRSHECIIDEDCGPSMYCQFASFQYTCQPCRQMLCTRSECCG
DQLCVWGHCTKMATRGNSGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASCGLLCQPHSHSLVYVCKPTFVGSRDQDGIEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEMALGEPEAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

FIGURE 86

MRLLVAPLLLAWVAGATATPVVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDFLTA
VPPALPAGTQTLLQSNSITVRVDQSELGYLANLTLDLSQNSFSDARCDPHALPQLLSSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRLSLVLAGMNLREISDYALEGLOSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKPLQRVGPQDFANMLHKLGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRFHHLPQMELTMLMNNNALSAHLQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPKSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPIYWVTPAGLRLTPAHAGRRYRVVPEGTIELRRVTAAEAGLYT
CVAQNLVGDATKTVSVVVGRALLQPGRDEQQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLTAILALAVLLAAGLA AHLGTGQPRKGVGRRPLPPAWFWGWSAPSVRVV
SAPLVLWPWNPGRKLPRSSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGGCCAAGGCGCTGTTTGAAGAAGGTGGAGAACGTCGGGACCCATTGGAGGAGGGGGACATTGTGACCGCCT
CTCATATGCCGAGACCATCATAAAGGTGATCAAGTTCATCTCATCATCTGCTACACCGTCTACTACCTGCAAA
CATCAAGTTCGACGCTGGACTGCACCGTGGACATTTGAGAGGCTGACGGGCTACCGCACCTACCGCTGTGCCCCACCC
CTTGCCACACTCTTCACATGATCTTCGCTCTTCTACATCAGCCTAGTCTATCTTACCGGCCATCTCGATGT
CACACTGTTGGTGTGACTGCTACGGCGCTCCTCAAGAAGTACTCTGTTGAGTCTGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCAGCAGCTCAAGAAGCAGTCTCCGCTTCAGCTGACCTTCTACCAAACTGAGCTTCTACTCCAA
GGCGCTTCGCCGCTCTTCTGAGGAGTGTGACTGAGAACAAAGCTGGGGCAGCTGAACCTCAAAACAGAGTGGAGCCT
GGAAGAAGCTCCCGCAGCGGCTCACCAAGAAGCAGGAGAAGCTGGAGCTGACCTTCTATGCTCAAGTGGCCT
CCCTGACACTGTGTTGAGCTGGTGGAGCTGAGCTGATCCCCGAGCTGACCATCCGGCC
CAGCATTCGCCAGCTCACGGGCTCACAGGAGCTGTGCTCAAGACACAGGGCCAAGATTGAAAGCCTGGGCT
GGCCATCTGGCGAGAGCTGGAGGAGCTGACAGGAGATCTACCGAGGAGATCTGGGCTGTGGATCTA
TAGCTCTGAAAGACACTGGAGGAGCTGACCTGAGCGGCAACCTGAGGCCAGAGAACACCGTACATCTGATCGA
CGGCGTGGGGAGCTCAAAAGCTCAAGGGTCTGGGCTCAAGAGAACACCTAACAGGAGCTGACGGCAGGGCTCT
AGATGTGGGGCTGACCTGAGAACAGCTGTCATCAAAATGGGGCACAAGCTCATGCTCTCAACAGCTCAA
GAAGATGGCGAACCTGACTGTAGCTGGAGGAGCTGCTGGAGGAGCATCCACCTCCATCTTGACGCT
CCACACGGGCTCACCTGCTTAAGCTGTGTTGAGCTAACACCATGCGTACATCCCCATCGAGATCGGCAACCT
CTGGAGGAGCTCTACCTGACCCAGAACATGAGGAGATCTGGGACCCAGGCTCTTCTACTGGCGAGCTGCG
CTACTGGGAGCTTCACCTGACCCAGAACATGAGGAGATCTGGGACCCAGGCTCTTCTACTGGCGAGCTGCG
GGCCACACTGGGAGCTTCACCTGACCCAGAACATGAGGAGATCTGGGACCCAGGCTCTTCTACTGGCGAGCTGCG
AGCCATCACGGGCAACCGGATCGAGAGCTTCCTCCGGAGCTCTTCAGTGGCGGAAAGCTGGGGCCCTGACCT
GGGCAACACGTCAGCTGAGCTACTGCCCTCCAGGGTGGGGAGCTGACCAACCTTGACGAGCTGAGCTGGGG
CAACGGGCTTGAGGTGGCTCTGGCTGGAGCTGGCGAGCTGCCACTGCTCAAGGGCAGGGCTTGTGGGGAGGA
GGACTCTGTAACAAACACTGCCAACAGGAGATCTGGGAGGAGCTGGGAGGGTGAACAGGAGCAGGCC
GCCGGGAGCACAGAACAGGGAGGAGCTGCCAGCTCAGGGGGAGGGGAGGGCTAGCTTCTCC
AACTCCGGACAGCGGAGACAGCTCGCGCTGGCAGGAGCTGGGGCCGCTGTGAGTCAGGGCAGAGGAGA
GGAGCAGTACTGTGGGGGCTTTCCTCTGAGACTCACGTCAGGAGCTGGGAGG
AGCAAGTCTCAAGGGCAGTATTGATAATCAGGGGCTCTCCCTGGAGGCTGAGCTCCCGAGGGCTGAG
CTGGCCACAGAGCTGGTGGGACCTACTTCTTGTGTTATTATTCTCCATCTCCACCTCTCATCC
AGATAACTTACATCTCCAAAGAACTTCAAGGGAGATGGAGGTGTTCTGAGGAAAGGTGGGCTGCGCTT
TTGCTCTTATTAGCGATGCCGCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAAC
CCATGGGAGCTGGGAGCTGGGGAGCTGGGGCTCTGGGCTACGGGAGAGCAGGCC
AAAGGGCAGGGCTGGAGCTTCTGGCTCTGGAGCTTCTGGAGCTTCTGGAGCTTCTGGAGCTTCTGGAG
AAACAACTTTTTTAAAGAAAAGCTTGGAAAATGAGTGGTTGGGTTTAAAGAAA
AAAAGACACTAACGGCAGCTGAGTTGGAGTCTCAGGGCAGGGTGGCA
TGAACTGTGTTCTCTTCCCTGGGGCCAGGGTGCAGGGTGTCTTCCCGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTGTTCTGGGGAGGGAGGTTTTTGTGTTTGGGTTTTGGGTCTTGTGTTCTTCTCTCC
ATGIGTCTGGCAGGGACTCATTTCTGTGGCTCTGGCAGAGGGAA
ACTCGGGTTGGCTAATCCCCGGATGAGCGGTGCTCATTGCACTCCCTCTCGTGCCTGGCTCTGGCTCTCCA
CGCAGTGGCACCCTGGCCCTGGCTGCTTCCATCAGGCCCTGCGCACCTGGCTTCT
GGGGCTGGGGAGGAGCTGGGGAGGAGCTGGGGAGGGAGCTGGGCTT
CTGGAGGTGACACAGGGCAGTGCGCACCTGGTGGCTGAGGCAACCTGCTT
AGATACTCTGGGGTCCCTGGCTTCAAGGAGCAGCTTAAAGGAGCAGT
CCATCGGTCTGTCGGCTATTGTTCTGGCTCTGTCATTGGATA
CCATCTGACAACCATGAAGAAAAAATCGGTTACATGTGGGCTGTGAA
ACTGTAGACTCGTCAAGCTACAGTATCAAA
ATCTATAACAGAAAAAAA

FIGURE 88

MRQTI I KVIK F I L I I C Y T V Y Y V H N I K F D V D C T V D I E S L T G Y R T Y R C A H P L A T L F K I L A S F Y I
S L V I F Y G L I C M Y T L W W M L R R S L K K Y S F E S I R E E S S Y S D I P D V K N D F A F M L H L I D Q Y D P L Y S K
R F A F V F L S E V S E N K L R Q I L N L N E W T L D K L R Q R L T K N A Q D K L E L H L F M L S G I P D T V F D L V E L E V
L K L E L I P D V T I P P S I A Q L T G L K E L W L Y H T A A K I E A P A L A F L R E N L R A L H I K F T D I K E I P L W I
Y S L K T L E E L H L T G N I S A E N N R Y I V I D G L R E L K R L K V I R L K S N L S K L P Q V V T D V G V H L Q K L S I
N N E G T K L I V L V N S L K K M A N L T E L E L I R C D L E R I P H S I F S L H N L Q E I D L K D N N L K T I E E I I S F Q
H L H R L T C L K L W Y N H I A Y I P I Q I G N L T N L E R L Y L N R N K I E K I P T Q L F Y C R K L R Y L D L S H N N L T
F L P A D I G L L Q N L Q N L A I T A N R I E T L P P E L F Q C R K L R A L H L G N N V L Q S L P S R V G E L T N L T Q I E
L R G N R L E C L P V E L G E C P L L K R S G L V V E E D L F N T L P P E V K E R L W R A D K E Q A

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Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCCGT
CCCGCGGTGGTGTGCTGCTGCCGTGCTGCGGTCTGAACGCAGGAGCTGTATTGACT
GGCCCACAGAGGGAGGGCAAGGAAGTATGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGTCCAGGCTGCCAGTCTCTATT
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAGGA
CCTGGCTATGGGGCTTCAGACATGATGGTCTCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTCCATTCTACATTTCTCAGAGTCTATGGAGGAAAATGGCAGTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCAGGGACCATCAAGTGAACATTGCGGGGT
TGCCCTGGGTGATTCTGGATCTCCCTGTTGATTGGTCTCTGGGACCTTACCTGT
ACAGCATGTCTTCTCGAACAGACAAAGGCTGGCAGAGGTGTCTAAGGGTGCAGAGAACAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACTTCTATAACATCTTAACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGCTAGAATTCACACAGGCACCTAGTTGCTTGTCAAGC
CACGTGAGACACCTACAACGAGATGCCAACAGCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAATTATTCTGGAGGATCAATCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACCAGGGTCAGGAGGCTG
GGTGGCGAAACTGAAGTGGCAGAACACTGCCCTAAATTCAAGTCAAGTGGCTACAAAGAAC
CTTGTCAAGTGGCTTGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT
TACTGGATTCTGAAAGCTGGTCATATGGTCTCTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGACAGAGGATAAAATCATTGCTCT
GGAGGCAATTGGAAATTATTCCTGCTTCTTAAAAAAACCTAAGATTTTAAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALARSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPVMWLQGGPGGSSSTGFGNFEEIGPLDSLKPRTTTLQAASLLFVDNPVGTFGSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GТИКCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGGLAEVSKVAEQVLNAVNGLYRE
ATELGWKAEMIIEQNTDGVNFYNIITKSTPTSTMESLLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVNGQLDL
IVDTMGQEAWRKLKWPELKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMLRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATCGTGGGTGGAGAGGACGCCA**A**CTCGGGCGTTGGCGTGGCA
GGGGAGCCTGCCCTGTTGGGATTCCCACGTATCGGAGTGAGCCTGCTCAGCCACCCTGGG
CACTCACGGCGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGGCCCTGC**T**ACCTGGGAATTCAACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACACTAAACACATCCAGCCATCTGCTCCAG
GCCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGC**A**CTGCCATCCCCAACCCCTCCAGGAAGTTCAAGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTCCGAAGGACATCTTGGAGACATG
GTTTGTGCTGCCAACGCCAACGGCGGAAGGATGCCCTGCTCGGTGACTCAGGTGGACCCCTT
GCCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCACTTGAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTC**C**AGCCAGACCCCTCTGCCACTACTCTTTCCCTCT
TCTCTGGGCTCTCCC**A**CTCTGGGCCGGT**TG**A**G**CC**T**ACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTCTCTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCCTTGAGGGCATTCTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLARAGLRKPEQEAAPLSGPCGRVRITSRIVGGEDAELGRWPWQGSRLRW
DSHVCVGVLSSHRWALTAACFCETYSDLSDPGWMVQFGQLTSMPFWSLQAYYTRYFVSNI
YLSPRYLGNSPVDIALVJKSAPVTYTKHQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVAINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSSGPPLACNKNG
LWYQIGVVSWVGVCGRPNRPGVYTNISHHPEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263.

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCCACCGCTCCGGGACCGCTGGGAAGGGCAGAATGGGACTCCAAGCCCTGCCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCGAGCCGACCAGCGAGGACGC
TGGCCCCCAGGCTGGGTGTCCTGGCCGTGCGGACCCCTGAGGAAGGCTGAGTCACCTTT
GCCCTGAGACAGCAGAAATGTTGAAAAGACTCTCGGAGCTGCTGCAAGGCTGTGCGGATCCCAG
CTCTCCCTAATAACGGAAAATACCTGACCGCTAGAGAAATGTGGCTGATCTGGTGAAGGCCATCCC
CACTGACCCCTCACACGGTGCAAAAATGGCTTGGCACCGGAGCCAGAACAGTCCATTCT
GTGATCACACAGGACTTCTGACTTGTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCTCATCACTATGTGGAGGACCTAGGAAACCCATGTGTAAGGTCCCCAC
ATCCCTACCGCTTCACAGGCTTGGCCCTATGGACTTTGTGGGGGACTGCCAGGT
TTTCCCCAACATCATCCCTGAGGCAACGCTGAGGCCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCTCTGTGATCGTAAGCGATAACAACCTTGACCTCACAAAGACGTGG
GCTCTGGCACCGACAATAACAGGCAAGGCCAGGCTGGCCAGTCTCTGGAGCAGTATTCATGAC
TCAGACCTGGCTCATGGCTCATGGCTCTCGGTGGAACATTGTCACATCAGGACATCAGTAGC
CCGTGTGGTGGACAACAGGGCCGGGGGGGGGGGGGGGGATTGAGGCCAGTCTAGATGTGAGT
ACCTGAGTGAATGGCTGGTGGCAACATCTCACCTGGGTACAGTAGGCCCTGGCCGATGAG
GGACAGGAGCCCTTCCTGAGGCTCATCTGCTCAGTATGAGTCAGGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGGCCCTACATCCAGGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTGGGTCTACCCCTCTTCGCTCAGGTGACAGT
GGGGCGGGTGGTGTCTCTGGAAAGACACCAGTCCGGCTTACCTTCCCTGCCCTCCAG
CCCCATGTCACCAACAGTGGGGCACATCTTCCAGGAACCTTCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGTGGCTCAGCAATGTGTTCCCACGGCCTTCATACAGGAG
GAAGCTGTAACCGAAGTCTCTGAGCTCTAGCCCCCACCTGCCACCATCAGTTCTCAATGC
CAGTGGCGCTGCCCTACCGAGATGTTGGCTGCACTTCTGTGACTGGCTACTGGTGGTCA
GAAGTGGCCATTCCATGGGTGTCGGAAACCTGGCCCTACTCCAGTGTGGGGGATCCTA
TCCTGATCAATGAGCACAGGATCTTAGTGGCCGGGGCTTGTGATGTAACCGTGGCTG
GCTCTACACAGCACGGGCTGGGCGAGGTCTCTGGATCTGAGCTTCTGGGATCTGTC
TGGATGAAGAGGTAGAGGGCCTGGGTTCTGCTCTGGTCTGGGATCTGTAAACAGGC
TGGGGAAACCAACTTCCAGCTTGTGAGACTCTACTCAACCCCTGACCTTCTCATC
AGGAGAGATGGCTGTGCCCCCTGCCCTGAAAGCTGGCAGTTAGTCCCTTATTCGCCCCGGTTG
GAAGGCGCTGCTGAACCCCTCAACTTGTACTGCTGAGACAGCTTATCTCCCTAACCTGGAAA
TGTCTGTGAGCTTGTACTGACTCCAAACCTTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCTCTAGATTCCTCAATAAGATGCTGTAACTGATTTTTGAATGCTCTCCCTCCGC
ATCTCATCTTCTCTTCTCAATCAGGCTTCTTCAAAGGGTGTATACAGACTCTGTGACTA
TTTCACTGTATTCATTCCCAATTCACTGCAAGGAGACCTCTACTGTGACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAAATGGCCTCCAGTGCAACTTCTCAATCTTGT
GCCCTTCCATCATAGTGGCCCACTCCCTCTCTTACTTAGCTTCCAGGTCTTAACCTCTCTG
ACTACTCTGTCTTCTCATCAATTCTGTGTTCTCATGGAATGCTGACCTTCATTGC
TCCATTGTAGATTGGCTCTTCTCATGTTACTCATGGTCCCCCTGGAACAAATCACTGACA
TCTACAACCAATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACTCAAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSFTALRQQNVERLS
ELVQAVSDPSSPQYGYLTLENVALVRSPSPLTLHTVKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHPYQLPQALAPHVDFVGLHRFPPSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGRDGGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPLITNEIVDYISGGGSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDDEVEGQGFCSGPGWDPTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCCGGGCCACACCTGTCAGGGCGCAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGTGTCGGCATGGCAGGGATTCCAGGGCTCTTCCCTC
TTCTTCTGCTCTGTGCTGGCAAGTGAAGCCCCACTGCCCCCTGGAAACCACTTG
GCCTGCATAACCGCCTCTGTCGCTTGCAGTCAACCTCAATTAGCCAAGCCAGACT
TTGGAGCGAAGCCAATTAGAAGTATCTCTCATGTGGACCCAGTGTCAAGGAACT
CCACTGCCCACCTACGAAGAGGCCAACGAAATCTGTCTTATGAAACGCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCAAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTGAAGGAAGGGCAGATTTATGGCTATGACAGC
AGGTTCACTGATTTGGAAAGGACTCCTGTCAACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGCAGAGAACGATGCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAGGAACCCAGAACGCTTCAGTGAGTGGCTTCCTAAAGCCC
AAGTTAAAGATGGTGGCGAGGGGCCAACGACTCCACTCAGCCATGCCAGCAGATGAA
ATTCAGTGGATCCGGGTGAAACGACCCATGTGCCAACGGTTGGATCAAGGGCAATGCCA
ATGACATCGCATGGATTATGATTATGCCCTCTGGAAACTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATGGGGTGAAGCCCTCTGCTAAGCAGCTGCCAGGGGCCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCCAGGAATTGGTGTATGCCCTCTGTGACGTCAGACGAGA
CCTATGACTGCTCTACCAGCAATGCGATGCCAGCCAGGGGCCAGGGCTCTGGGCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGAACACAGTGTCCCTCTGGCAGCAATTAAAGGTCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTGTCAATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGAAGGTGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTTAACGAGTTGAAGGCATACTTTGCATAGAAAATAA
AAAAAAACTGATTGGGCAATGAGGAATTGACAATTAAAGTTAATCTCACGTTTG
CAAACTTGATTTCATCTGAACCTGTTCAAGGATTATTAATTTGGCATA
CAAGAGATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
SSCGPQCHKGTPPLPTYEEAKQYLSYETLYANGSRTE
RRKRQIYGYDSRFSIFGKDFLLNYPFSTS
TQKLRVGFLKPKFDGGRGANDSTS
LLELKPKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNL
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNV
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGTCTCTGAGCCTGCTGCCGTCTCCCCGCCCCACCAAGCC**ATGGTGGTT**
CTGGAGCGCCCCCAGCCCTGGTGGGGCTGTCCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACTGTTCCCCCAGCCTGTGGAGGCCA
GCAGCTGAACCAGGGTGTGGCGGCAGGACAGCAGCAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAAATGGGACCCACCACTGCGCAGGTTCTGCTCACAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGCTGCTGGG
GGCCTGGCAGCTGGGAACCTGGCTCTGGTCCCAGAAGGTGGGTGTGCTGGTGGAGC
CCCACCCCTGTGATTCTGGAAAGGAAGGTGCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCTCACCTGATGCCCTATCCACCT
CCCTCCAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTG
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTAAGTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCGGCTACTT
GGAGGGGAGCGGGATGCTTGTCTGGGCACTCCGGGGCCCCCTCATGTGCCAGGTGGAGC
GGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGGTGGAGAAGATCGTGAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCAGGGCTCTGGGCG
CCGCGCGCT**CTTAAGGGCGCAGCGGACGCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA**
TCTGGATCTGGATCTGCGGCCGCTCGGGGGTTCCCCCGCCGTAATAGGCTCATCTACC
TCTACCTCTGGGGCCCGGACGGCTGCTCGGAAAGGAAACCCCTCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGGCCCGCCAAAGGCCCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGCCCCCGGGCCCCAGCCCTTTGTGTATATAATGTTAATGATTTTAT
AGGTATTGTAACCTGCCACATATCTTATTATTCTCCAATTCAATAATTATTATT
CTCCAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTCSRWWITAHCFKDNLNKPYLFSVLLGAWLGNPGRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALARPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCACATGCACGGCTCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCACACAGGGCCCGTTGGAGCCTCACAGATGAGGAAGAAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAAGGTATCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCTTCGCAAGGCCTACGCAGGCAGTGCGTGGGCCAC
AACAGGAGCCGGCGCCGCGGAGAACTGTGCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACACGAGCTGAGCACTACAACTCAGCGCCCCACCT
GCAGCCCAGGCCAGATGTGCGGCACTACAGCAGGTGGTATGGGCAAGACAGAGGAGTC
GGCTGTGGTCCCACTTCTGTGAGAAGCTCCAGGGTTTGAGGAACCAACATCGAATTACT
GGTGTCGAACTATGAGCCTCGGGGAACGTGAAGGGAAACGGCCCTACCAGGAGGGACTC
CGTGCTCCCAAGTGCCCTCTGGCTACCACTGCAAGAACCTCTGTGGAACCCATCGAACG
CCGGAAAGATGCTCAGGATTGCCTACTGGTACTGAGGGCCCATCTTCCGGGCACTGA
AGCATCGACTCTAGGAAAATGGTACTCTTCTCCTAGCAACGGGATTCCGGCTTCT
TGGTAACGAGGTCTCAGGCTCCGGCAACAAGGCTCGCTGTGGGAAACCCAGGCC
CCAACTCTTTAGCAAAGACCCGGCCCTCAGGCAACAGAGGCTCCACTTGGTAAC
AACTGAGGCTCCTTCCATTGGCAGTCTACAGGCTCCCTCCTTGGATGAGGAGCCAGTT
CTCCTTCCAATCGACCATGGCTCCATCCAAATCGAGACAAAGGTGAAGAAACA
AAAGTGCCCCTAGGGAGCCAGGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACTCCTACCCCATGGCCAGGGAGGGCTGTGAGGGCTGTGAGGGTTGCCTCCTTCCAGGT
AGGTCTGGCCTCAGTTCCAGCCAGGAAAGGCCAGGTGAGCTGCAGGGCCACACTGGAC
CAACGGGGCAACCCCTCCCAAGCTCCGTCCAAATTTCCCAATACCTGCCCACCGCTAA
TGCCACGGGTGGCGGTCCCTGGCTCTGCAGCTGTCCTTGCAGGGCCCTGTAC
AGCCCTAGCGTTGTGTCAGGCTGACTGGCCCTGGCTATGTGTGGCCCTCTCCGGGA
CTTACTGTCCCTGCCTCCCTGGGTGGGTGGAAATCTCTGTGAATGGATACCCACCTCAAAAGGG
TGGAAGGGCTAGCTGTCCCTGTCATCTTCCACCCCTGTCCCCAGCCCTAAACAGATA
CTTCTTGGTTAAGGCCCTCCGGAAAGGGAAAGGCTACGGCCATGTGCCTCATCACCCATCC
ATCCGGAGGGCAACGGCTGGCTGGCTGCAGCTCAGGAGGGCCCTGTAGGACTGCACCC
GGGGCCACCCCTCCCTGCCCCTCCCTCCGTAGCTGTGGGGGTGGGAGGATTTGAGGGAGT
CACTGCCTACCTGGCCCTGGGTGTCTGCCCACAGCAGTGTGCCGCTCCCTGAGTGCCTGG
TGTGAGGTGGGGATGGGTGGATCCTAGGGGCAGTGAAGGGACAAGGCCCACTGGAGGTGGGTTC
TTTGAGGTGGGGATGGGTGGATCCTAGGGGCAGTGAAGGGACAAGGCCCACTGGAGGTGGGTTC
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLWATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVCWGHNKEGRGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAACSPGQ
MCGHYTQVVAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPYQEGLPCSQC
PSGYHCKNSLCPEIGSPEDAQLPVLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLGAEGPDKPSVV
SGLNSGPGBHVWGPLLGLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLSSLGNRIVEILP~~E~~HLEKFQSLETLDLSSNNISELQTA~~F~~PA~~L~~QLKLYLNSNRVTSMEP
GYFDNLANTLVLKLN~~R~~NR~~I~~S~~A~~IPP~~K~~MF~~K~~L~~P~~QLQH~~L~~ELRN~~R~~N~~K~~IKNV~~D~~G~~L~~T~~F~~Q~~G~~L~~G~~ALKSLKM
QRNGVT~~K~~LM~~D~~GAFWG~~L~~S~~N~~MEI~~L~~QLDHN~~N~~LT~~E~~TKGWL~~Y~~GL~~M~~Q~~E~~LHLSQN~~A~~INR~~I~~SPDAWE
FCQKLSEL~~D~~LT~~F~~NHLSRL~~D~~SS~~F~~LG~~L~~SL~~M~~NTLHIGNNR~~V~~SIADCA~~F~~R~~G~~L~~S~~SLKTLDLKNN~~E~~
ISWTIEDMNGAFSGLDKLRL~~L~~IQGNR~~I~~R~~S~~ITKKAFTG~~I~~DALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLH~~L~~NTSSLLCDCQLKWL~~P~~QWVA~~E~~NNFQS~~V~~N~~A~~CAHPQLLKGR~~S~~IFAVSPDG~~F~~VCD
DFPKPQ~~I~~TV~~O~~PETQSAIKGSNL~~S~~FC~~S~~A~~S~~SSD~~S~~PM~~T~~FAWKKD~~N~~ELLHDAE~~M~~ENYAH~~L~~RAQG
GEVMEY~~T~~TLRLR~~E~~VEFA~~S~~EGKYQC~~V~~CV~~I~~SNH~~G~~SS~~S~~SV~~K~~AKL~~T~~VNMLPSFTKTPMDLT~~I~~RAGA
MARLECAAVGH~~P~~APQIAWQKDGG~~T~~FP~~A~~RERRHM~~H~~VM~~P~~EDDVFFIVDV~~K~~IEDIGV~~S~~CTAQ~~N~~
SAGSISANATL~~T~~VL~~E~~TPSFLR~~P~~LLDR~~T~~VT~~K~~GETAVLQC~~I~~AGGS~~P~~PP~~K~~LNWT~~K~~DDSP~~L~~V~~V~~TER
HFFAAGNQLL~~I~~IVD~~S~~DS~~V~~DA~~G~~AKY~~T~~CM~~S~~NTLG~~T~~ERGNVR~~S~~VIPTPTCDSPQM~~T~~APS~~L~~DDDG
WATVG~~V~~V~~I~~IAV~~V~~CCVV~~G~~TS~~L~~W~~V~~V~~I~~YHT~~R~~RRNEDCS~~I~~TNTDETNLP~~A~~D~~I~~PSYLSQ~~G~~T~~L~~AD
RQDGYV~~S~~SESGSHHQ~~F~~V~~T~~SSGAG~~F~~FLPQHDSSGT~~H~~IDS~~N~~SEAD~~V~~EAT~~D~~FLCP~~F~~LG~~S~~T~~G~~P
MLKGK~~V~~RL~~N~~NTSY~~H~~NE~~G~~PGM~~K~~N~~L~~C~~N~~K~~S~~LD~~F~~SAN~~P~~EPASV~~A~~SSNS~~F~~M~~G~~T~~F~~G~~K~~ALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGS~~E~~EDG~~K~~ERTDFQ~~E~~BNHICTFKQTLEN~~Y~~RTPNFQS
Y~~D~~LD~~T~~

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLIEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKEWLRLNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCAMCNLREIPNLTPLIKDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNLTLLPHDLFTPPLHHLERIHLHHNPWNCCNDIL
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVNSVGN
TTASATLNVTAAATTTPFSYFSTVTETMEPSQDEARTDDNNVGPTPVWDETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIIINVDDIEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELQPSGVAERPCTTCRCLGDLDDCSR
KRLARLPLPEPLPSWVARLDLSHNRLSFIAKASSMSHLQSLEVKLNNELETIPNLGPVSA
LLSLLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLIANTLLVTLNLRNRIASIAPKMFKLPLQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMDFGFWGLSNMELIQLDHNNLTEITKGWLGYGLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLDDLKNNEIS
WTIEDMNGAFSGLDKLRRRLIQLQGNRIRSIKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQQLHLNTSSLCDCKLWKLPQWVAENNFSFVNASCAPOLLKGRSIFAVSPDGFVCCDF
PKPKQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAGG
VMEYTTILRLREVEFASEGEKYQCVCISNHPGSSYSVAKLTVNMLPSTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGTDFFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCATAQNSA
GSISANATLTVLETQPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSPVTERHF
FAAGQNLLIIVDSDVSDAGKYTCEMSNTLGTTERGNVRLSVIPTPTCDSPQM TAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSQGTLADRO
LKGNVYSESGSHHQFVTSSGFFLPQHDSSGTCHIDNSSEADVEAATDLFCPFLGSTGPMY
HVRKLLNNTSYHNEGPGMKNLCKLNSKSLDSANPEPASVASSNSFMGTFGKALRRPHLAYS
SFGQPSDCQPRAFYLKAHSSPDLSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYQLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

FIGURE 108

MEGEEEAEQPAWFHQWPWRPGASDAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENFAEEEPVLVLSPPEEPGP GPAVSCP RDACS QEGVVD CCGI DLREF PG DLP
EHTNHLQLQNNQLEK IYPEELSRLRHLT LNLQNNR L TS RGL P EKA FEH LTN LYLA NNK
LT L A PRFLP NALIS VD FA A NYLT KI YGL TFG QKP NLRS VY LHNN K LAD A GLP DNM FNG S NV
EV LILSSN FLR HVP KHL P ALY K LHL KNN K L E K I PPG A FSE L SS L RE LY L QNN Y LT DE G LD N
ET FWKL SS LEY LD LSS NN L SR VPAG L P R S L VLL H L E K NAI R S VD AN VLT PIR S LEY LL HSN
Q LREQGIHPLAFQGLKRLHTVHLYNNALERPVPSGLP RVR TLMILHNQITGIGREDFATTYF
LEELNLNSYNRITS PQVHRDAFRKLRLRSLDLSGNRLH LTPPGLP RVN VHVKV KRNEAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLT EPI EGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSA FRR LKHLQVL DIEGNLEFG DISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCPD
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDDVVKGGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCRFRQC
VNIFGSYICKCHKGFDLMIIGGKYQCHDIDECSLGQYQCSSFARCYNRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHPKGNGTILKGDTGNNNWIDPVGSTWWPPKTPYIPPIITNRP
TSKPTTRPPTPKPTPIPTPPPPPPLPTELRTPPTTPERPTTGLTTIAPAATPPGGITVDN
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAQQYLTVSAAKAPGG
KAARLVLPLGLRMHSGDLCLSFRHKVTGLHSGLQVFVRKGAHGAALWGRNGGGHWRQTQI
TLRGADIKSEQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

09932853 - 071004

FIGURE 111

CTTCTTGAAAGGATTATCACGTACGGTTCTCTGCATTGCCCTTAGATTGTGA
~~AATG~~TGGCTCAAGGCTTCACACTTCCCTTGACAGGCTCGCTCGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCTCAGAGGTAGGGCTTACCTACCGTC
CACTATGGCTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCCA
ACAATGCCAAATCTTACTGGGCTCTGTGAATAAGTCGTGGTCTGACTTGGAAATACC
AACACAAGTTCACCATGATGCCACCAAATGATCTCTGCTTACACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTAAGGTCACAACTCAGGGAAATGGAACACTATCTGCCAGTCA
GAAGATAACAGTCACGGTTGATGATCCTGACAAAGCAGTGGTCAAGATTACATCCCT
CTGGGCTGTGGAGTATGTGGGAACATGACCTGACATGTGGAAAGGGGGCACTGG
CTAGCTTACCAATGGCTAAAATGGAGACCTGTCCACACCAGCTCACCTACTCCTTTC
TCCCCAAACAAATACCCCTCATATTGTCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCCTGGTGAAGGAAACCTCTGCTAGTGAATGGAAGTGTATCATTATGCCACATCATATTAT
GGACCTTATGGACTTCAGTGATTCAGTAAAGGGCTAAAGGGAAAGTGTATTACTGT
TGACCTTGGAGAGGCCATCTTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CTCTGGATTAGGAGGACTGACAATACATATATCATTAAGCAGTGGGCTCGCTTAAAGGTT
GCATCTGAGAAAGTGGGCAAGAACATGGACTATGTGCTGTGCTTACAAACACATAAC
CGGCAGGAAGGAAACTCATTCCAGTATCATCCTCCGAGGACTGGAGAAGCTTG
CACAGAAAGGAAATCATTGTCACCTTAGCAAGTATACTGGAATATCACTATTGGATT
ATATCCATGTCTTCTCTCTGAAATGGAAAAAAATACACCTCAAAGTTAAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTGGAAATATATGAATTGTTGCTTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTTATCGGGCAAGATTGACAGTACAGT
GTATGAAGGTTATTAGCACATCCCTGCCAGCAGCAAGGACATCCAGAGTGAACCTTCATGG
GCTAAACAGTACATTGAGTGAATTCTGAAAGAACATTGTTAGGAAAACAGTGGAAAAGT
ATATTAAATCTGGAATCAGTGAAAGAAACAGGACCAACACCTTCACTATTATTCTTACA
TCCAGAAATAGGGCATTATTGCAAATTGAACTGCAGGTTTTTCAGCATATAACACATGCTT
GTGCAACAGAAAACATGTTGGGAAATTATTCTCAGTGGAGAGTCTTCTCATGCTGACGG
GGAGAACGAAAGTGCACAGGGTTCTCATAGTTGTTGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGCTCACCTACAA
TGTGGAAAACCTTACATTGTTGATTTTCAGCAGACTTTGTTTATTAAATTTTATTAGTG
TTAGGAATGCTAAATTATTGTTCAATTATTCCAAATTCTATCTGTTATTGTACAA
CAAAGTAATAAGGATGGTGTCAACAAAACAAACATGCTTCTCTTTTTCAATCACC
AGTAGTATTGGAGAGACTTGTGACACACTTAAGGAAATGACTATTAAAGTCTTATTTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTCTGTTTGCTTTAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGTLSASQ
KIQVTVDPPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEIDIGNYSLRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLLEVASEKVAQKTMGYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEVFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAAATGGGCCCTCCGGGAGTCTTCGAGTCCCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGCCTCCCTGGACGCACGGGGCGGAGCACGTCGCGTCATCACGGACGAGA
ACTGGAGAGAACCTGCTGAAAGGAGACTGGATGATAAGAATTATGCCCGTGGTCCCTGCT
TGTCAAATCTCAACCGGAATGGAAAGTTTGCTGAATGGGAGAAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAATGGACGGTTATCATACGTCTC
TTCCTACTATTATCATTGTAAGATGGTGAAATTAGGCCATACAGGGTCCAAGGACTAAAG
AAGGACTCTATAAACTTTAAAGTGTAAAGAGTGGAAAGAGTATTGAGCCCGTTCATCATG
GTTGGTCCAGGTTCTGTCAGTGTAGTATGTCAGCACTCTTCAAGCTATCTATGTGGA
TCAGGACGTGCACTAACTTTAAGACCTGGATGGCAGTGGGGATCATATACT
GTTTTGCTTGAACACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATAATTGTGGC
AGATTGCTTGTCTCAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAGGAA
TATTATCAGAACTCTGACACACCTTGAAAGAAAGTGGAGGAGAACAGAGGGCGGATGAAGAA
GATGTTCTCAGAGAAAGCTGAAAGTAAAGAGAACAAACAAGACTTCCACAGAATGC
CATAAAGACAACGCTCTGGGTCATCATTGGCACAGATAATCTAGTTAAATTATAG
TTATCTTAATATTATGATTGATAAAAACAGAACGAGATTGTCATTGGTTGGTTGAAGGTG
AACTGTGACTTTTGATATTGCAAGGGTTCAGTCTAGATTGCTATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATTGATTTAGCACAGTATGATG
GTTAAATAGTTCTCTAATTTTGAAAGATCTGTCAGCAAGCAATAAGATTATGTTATTTGT
TTAATAAACTATTTCAGTCTGAGTTGAAAGATTCTCAGTCTGATTTCAGTCTTCAATT
TGAGGTTATTAAAGAAGATTTTAGGAAAAAATTTCTCATTTGATAATAATTCTCTG
TTTCACTGTGAAAAAGAACGATATTCCATATAATGGGAAGTTGCCATTGTCAG
AAATGTGTTATTCACTGTGACATACTTCTGTCATTAGAGGTATATTCCAAAATTCTCTGT
ATTTTAGGTTATGCAACTATAAAAACCTACCTTACATTAATTACAGTATTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCTGATTGTTACATTCCAGT
CAACAAAGTTGATTTCTCTGTATTCTACTATGGGTTACATTTTTATTGTT
CAAATTGGATGATAATTCTGGAAACATTTTATGTTAGTAAACAGTATTGTT
GTTCTAAACTGAAGTTACTGAGAGATCATCAAATTGAAACATCTGTGTAATTAAAATT
TTGCCACTTTTCAGATTACATCATTCTGCTGAACCTCAACTGAAATTGTTTTT
TTCTCTTTGGATGTAAGGTGAACATTCTGATTTTGCTGATGTTGAAAAAGCCTGGTA
TTTACATATTGAAAGCTTAAAGACTTAAATGTTCTCTCATACAGAAAGTTCTAATTGAT
TTTACAGTGTGAAATGCTGATGTTTAAATAACATTTTATATTAAAAGACAA
ACTTCATATTCTGCTCTCTGACTGGTAATTGTTGTTGAACTTCAACAGTAAAAA
GTCAGTAGGATGGAACATTAGTGTATTCTACTGCCCTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGGAAATCATAAATACAATGAATCAACTGACCAATTACGTAGTAGAC
ATTCTGTAATGTCCTCTTCTAGGCTCTGTCGCTGTAATCATTAGATTACAG
TATCGTAATACAAAGTTCTTAAAGCCCTCTTAAAGGCTCTCCTTGAATTAAATATTGTA
AAAGAGTTGGATGTTGAACTCTGATGCCCTAGAAAAAATCTCTAAAGCACAAAATAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRPQPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNPAIRQRSLGPSSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

0990202853 071001

FIGURE 115

GGAGTGTCCAGCTGCGGAGACCCGTGATAATTCTGTTAACATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAACCGCAAGCAGTGTGACACTTCCCTGTGACC**ATGAA**CTCTGGGTGCTGC
AAGTCCTGCCAGAGCAGTGTGACACTTCCCTGTGACC**ATGAA**CTCTGGGTGCTGC
ATTGCTGATGGCTGGTTGGTCTGAGCTGTGCAAGGCCAATTCTCACCTCTATTG
GCCACATGACTGACCTGATTATCAGAGAACAGACTGTCAGTCTGAAAGAGTACATC
CTTGAGGAGGAAGCCAAGCTTCAAGATAAGAGCTGGGCAACAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGTACCTGGCTCACCTGTGAATGCTACAAACTGG
TGAAGCGGCTAACACAGACTGGCTCGCTGAGGCCATTGCTCTGAGGACTCAGCTGCA
GGTTTATCGCAACCTCTCGCAGCGCAGTCTCCCCACTGTAGTGGAGCAGAGATAGG
ACGTGCCAACGCCCTGTAGGAGACTTCAGGACACATACAGGCTGGACCAAGGACAATTCCA
GAGGGAACTTCCAGGAACCAAGTACAGGAATGCTGAGTGTGGATGACTGCTTGGATG
GCCGCGCTAACATGAGGAGACTTATCATACAGGTGTTGGATGAGGAGCAGGTGCT
AAAGCAGCTTGTGATGCCGGAGGAGGCCAACCAAACAGGTCTGGACTAACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGACCGTGCCTGGAGCTCACCGCCCTGCTC
TCCCTGACCCAGGCCAACGAGCTGGAGGAATCTGGCTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAACCTTAACAAATCAGACAGAACGCTGAGCTAGAACCCCAGAGGA
TCTGAGAGGCCCTGTGAGACTACCTGCTGAGAGGATTTACGAGACCTGCTGCTGGG
GAGGGTGTCAAACGTGACACCCGTAGACAGAACAGGAGCTTCTGTAGGTACCAACATGCCA
CAGGGGCCAACAGCTGCTCATGGCCCTAACAGGAGGAGCAGTGGGACAGGCCGACA
TCGGTCAAGGTACTACGATGTCATGTCAGGAAATCGAGGAGTCAAGGAGATCCAAAAA
CCTAAACTTGCACGAGCCACCGTCTGTGATCCAAAGACAGGAGTCTCACTGTCGCCAGCTA
CCGGTTTCCAAAAGCTCTGGTAGAGGAAGATGATGACCCCTGTTGCCCCGAGTAATC
GTCGGATGCACTATCACAGGGTTAACAGTAAAGACTGCAAAATTGTTACAGGTTCAAAT
TATGGAGTGGAGGAGACAGTGAACCGCAGTCCACTTCTAGGGCACCTTTGACAGCGG
CCTCAAAACAGAGGGAAAGGGATAGTTAGCCAGTCTTCTTAACTACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACACCTCTGGAGGAGCAGGGAGGTGACTACCGAACAGACATGCTGCC
TGTGTTGTGGCTGCAAGTGGTCTTCAATAAGTGGTCTCATGAAAGGAGCAGGAGTTCT
TGAGACCTTGTGGATCAACAGAACAGTGTGACT**TGAC**ATCTTCTGTCCCTTCCCTGGTC
CTTCAGGCCATGTCAACAGCACCTTGTGATGTTCTGGAGCAGAGGGAGACCATACTAGGGCAGTCTGT
GATTTGGAGAAATGAATGTTGCTGGAGCAGAGGGAGACCATACTAGGGCAGTCTGT
GTGACTGAAGTCCCAGGCCCTCCATTGAGCTGTGCCATCCCTGGCCCAAGGCTAGGATCA
AAAGTGGCTGAGCAGAGTGTAGCTGTAGCCAGGTCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCACTGAACCAAAGTTCTGATACCTGTGTTACATGTTTGTGTTTAT
GCCATTCTATCTATTGTGGTTACCAAAAAATAAAATGCCCTACAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSVCVQAEEFTSIGHMTDLIYAEKELVQSLKEYILVVEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDPTYRLDPGTISRGELPGTKYQAMLSVDDCFGMRGSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFPEQOLLEEREKTLTNQTEAELATPEGIYERPVVDYLPERDVYESLCRKGEGVKLTPRRKRLF
CRYHHGNRAPQLLIAPPKEEDEWDSPHIVRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRRMQHITGLTVKTAELLQVANYVGQQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIPKKGTAVFWYNLLRSGEVDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCTCCCTTTAGGAAGACAGACATATCCAGTGAGTGAATGTGTT
TCATTTAACCGTTGGCTGGGGTAGTTCCGACACCTTCACAGTTGAAGAGCAGGAGAGATGTGA
AGACAGGACAATCTCTGGGGATGCTGGCTGGAGCAGCGGCTTGCTCTGCTCTGCTCTGGCTCATGACC
CAGTTCTCTGGTAAACTGAAAGCTACTACTGGCTCTGGCTGGCCATCAATCATTGATCCTTGAGGCTGTGCC
CTGGGCCCCACCCACTGGCAGGCCATACCCACATGCGACTGAGCTCCCTGCTCTGCTCTGCTCTGCC
CCCTCATCTTAAGGCTGCTCTGGGGTAGGGAGGGCACAGAATCCAGATTGAGACTCGCCTAGACCAAAGT
ATGAGACTTCAACCCGGATTGCTCCCTACTACAGGGACCCAAAGGCCATCAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCGTGCTGGCTGTCTGACCTCCCGAGGCTACACTGTCCA
CTTGGCGTGTGACCGTACGGCTGGCCATCACTTCCCTCGGTTACTCTACTTCACTGGGAGGGGG
CCCGGGCTCAGCAGGGATGAGCTGTCTGACGGGATGAGCGCCCGCTGGCTCATGAGACACCCTGC
GCCACCTTCACACACTTGGGGCCACTACGACTGTTCTCATCAGGATGACACATAATGECAGGCC
CCCGCTGCGACGCCCTGCTGGCACCTCAGCATCAACAGACCTACTTGGCCGGCAGAGGAGTCTT
GGCAGGGAGGAGGCCGACTGGCTTGGGGCTTGGCTACTCTGTGACGGAGTCTCCCTGCTGTGCC
GGCCACATCTGGATGCGCTGGCAGGAGACATCTCAGTCCCCTGCTGGAGCTGGCTTGGACGCTGCCATTG
ACTCTCTGGGGCTCGGCTGTCTCACACAGGGCAGCAGTACGCTCATTTGAACTGGCCAAAATAGGG
ACCCCTGAGAAGGGAGGAGCTCGGCTTCTGAGTCTTCCGCTGACCCCTGCTCCGAAGGGTACCTT
ACCGGACACTAACCGCTTACGGCTCTGGAGTTGAGGACGGGCTTACAGTAAAAATAGAACAACTGCA
TCCGGAACCTGACCGTGTGACCCCCAAGGGGAGGGAGGGCTGAGCTGGCCCTGGGCTCCCTGCTCTTCA
CACCAACACTCTGCTTGGAGGCTGCTGGCTGGACTACTTCACAGACGAGCACACCTTCCTGTCAGATGGG
CTTCCAAAGTGGCCACTACAGGGGGTAGCAGGGCGACGCTGGGTGAGCTGGGGAGACTGCCCTGGAGCAGCTCA
ATCCGGCGTATCACGGCCCTCGCTTCCACAGAACGGGACTCTCACCGCTATGCCGCTTGGACCCAGCAC
GGGCATGGAGTACACCCCTGACCTCTGTGTTGGAAATGTGAGCACACGGTGGGACCCGGGGCTTGTGCC
GGGTAGGCTCTGGGGCCACTTGAGGG
AGCTGCTCTGCCACTTGGGGCTGAAAGCTGCTCAGGCCCGCTTCTCTGAGGGGTTTGGCAGGCAATGTCC
TGGAGCCACGAGAACATGCTACCCCTGTTGGCTGGCTACGGGCCACAGAGAAGGTGGCGTGGAGACTCCAG
ACCCATTCTTGGGTGAAGGCTGAGCAGCGGAGTTAGAGCAGCTTACCCCTGGAGGCTGGCTGGCTCG
CTGTGCGAGCAGGGCCCTTCCAGGTGCGACTCAAGGCTGGGACCCCTGGGGGGGGGGGGGGGGGGGGGGGGGG
TCTTCCCTTACACCGCTGTTGGGACAAGGCTGG
GGCAGGCCCTTCTTCCAGTCAATTCTGCGCTGTCACCAACAGAGATACCCCCCAGGGGCC
GGGGGGCTGGCCCTGACCCCCCCCCTCCCTGTGCTGACCCCTCCGGGGGGCTCTATAGGGGGGGAGATTG
ACCCCGAGGCTCTCGGGAGGCTGTTCTCAACACCTGACTACTGGCGCCGGCAGGGCTGGCAGGTGAAC
TGGCAGGGCAGGAAGAGGGAGAGCCCTGGGGGGCTGGGGTGAATGGATGTTTCTCCGGGTTCTCAGGGCTCC
ACCTTTGGGCCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGGAGACTGAGCCACGGCTCAGTGAAG
AACTCTACCAACGGCTGCCCTCAAGAACCTGGAGGGGGTAGGGGGGGCTGGCCAGCTGGCTATGGCTCTCTT
AGCAAGGAGCAGGCCATAGCACTTAAGCCGCCCTGGGGGGCTAACCTTACCTTACCTTCTTGTCTGCCAGCC
CCAGGAAGGGAGGGCAAGATGGGAGAGATAGAGAATTGTTGCTATTTTTAAATATGAAAATGTATTA
ACATGTCCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNPKYKKVLRTTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVSHGDERPAWLMSETRHLHHTFGADYDWFFIGQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSSLRLRPHLDGCRG
DILSARPDEWLGRCLIDSGLGVGCVSQHQCCQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAIRNLTVLTPECEAGLSPVGLPAPFTPHSRFEV
LGWDYFTQHTFSCADGAKPCPQGASRADVGDALETALEQLNRRYQPLRFQKQRLNNGYR
RFPDARGMNEYTLIDLLECVTQRGHRRALARRVSLLRPLSRVEILMPYVTEATRVQLVLPLL
VAEAAAAPAFLEFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAEEELEERRYPG
TRLAWLAVRAEAPSQVRIMDVVKKHPVDTLFLTTVWTRPGPEVLRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPGAGPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAALEGLEVMVDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAACCGTGC~~GCGCTGC~~CTTCCGTCCCCAAGCC
GTTCTAGACGCCGGAAAAATGCTTCTGAAGCAGCTCCTTTGAAGGGTGTGATGTTGG
AAGCATTTCGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCA~~TGAA~~ATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAAGAAGATATCTTGA~~AA~~ATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGAGTAAGGAGACTGGACCAAA~~C~~ACTGTGACAAAGCAG
AGTTCTTCAGTTCTGA~~AA~~ATGTTAAAGTGTGAGTC~~A~~TTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCTTGTATAAGTATAGAGACCAATACAACTG
GTTCTTCCTGACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGCTTAAGTGTAGAA~~T~~ATGAAAGACTTAACAGCCTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTTGCAGAA~~T~~GCAGAAAGATGCTGATGGA
AAAGATGTATTAA~~T~~ACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTGTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGTATACCGCCTTAGGCATTGGCATATTTC~~CA~~AT
GATGCATTGGTTTCTTACCTCAAATGGCTGACAATGACTGAGAAGTGGTAGAAAGCG
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTAGTAGTAA~~C~~ATATCCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTCTTAAACACATGAACATTGTAATG
TGTTGGAAGAAGTGT~~TT~~AAAGATAATAATTGCAAA~~AA~~ACTATTAAATAATATTATAT
GTGATAAA~~T~~CTAAATTATGAACATTAGAAATCTGTTGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGC~~G~~TCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACCTTTAGCTGTGTTCCCTTA~~T~~CTAATGATT~~T~~ATGTTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCTCTCAAAATGTACA~~A~~CTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGT~~AA~~AT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDEILKISEDERME
LSKSFRVYCIILVKPKDVSLAAVKETWTKHCDKAEFFSSENVKVFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYLQFLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

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FIGURE 121

CCACCGCGTCGATCTTACCAACAAAACACTCCTGAGGGAAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAACCAAAGAGAGAGAAAAAATGAATTCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTCTCAGTGCTGTTCATCACAGATGTTGTGACATTTCGCAT
CTTCAAAACCTGTGATGAGAAAAAGTTCACTGAGAATTTCACAGAGCTCCTGCT
ACAATTATGGATCAGGTTCACTGAGAATTGTTGTCATTGAACTGGAAATTTCATCC
AGCTGCTACTCTTTCTACTGACACCATTCTGGCGTTAACGTTAAAGAACTGCTCAGC
CATGGGGCTCACCTGGTGGTATCAACTCACAGGAGGAGCAGGAATTCTTCCATAAGA
AACCTAAAATGAGAGAGTTTATTGGACTGTCAGACAGGTTGTCGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGGCCAACAA
CATAGCTACCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTGGATTTGTAATGGTAGGAATAATCCTTG
ACAAAGGAAATCTCTTAAGAACAGAAGGCACAACTCAAATGTGAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAA
AA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGGSVKNCCPLNWEYFQSSCYFFSTDТИSWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

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FIGURE 123

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPPLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAKSARCEEQEMEVYDLDNIGGIIGG
VLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267